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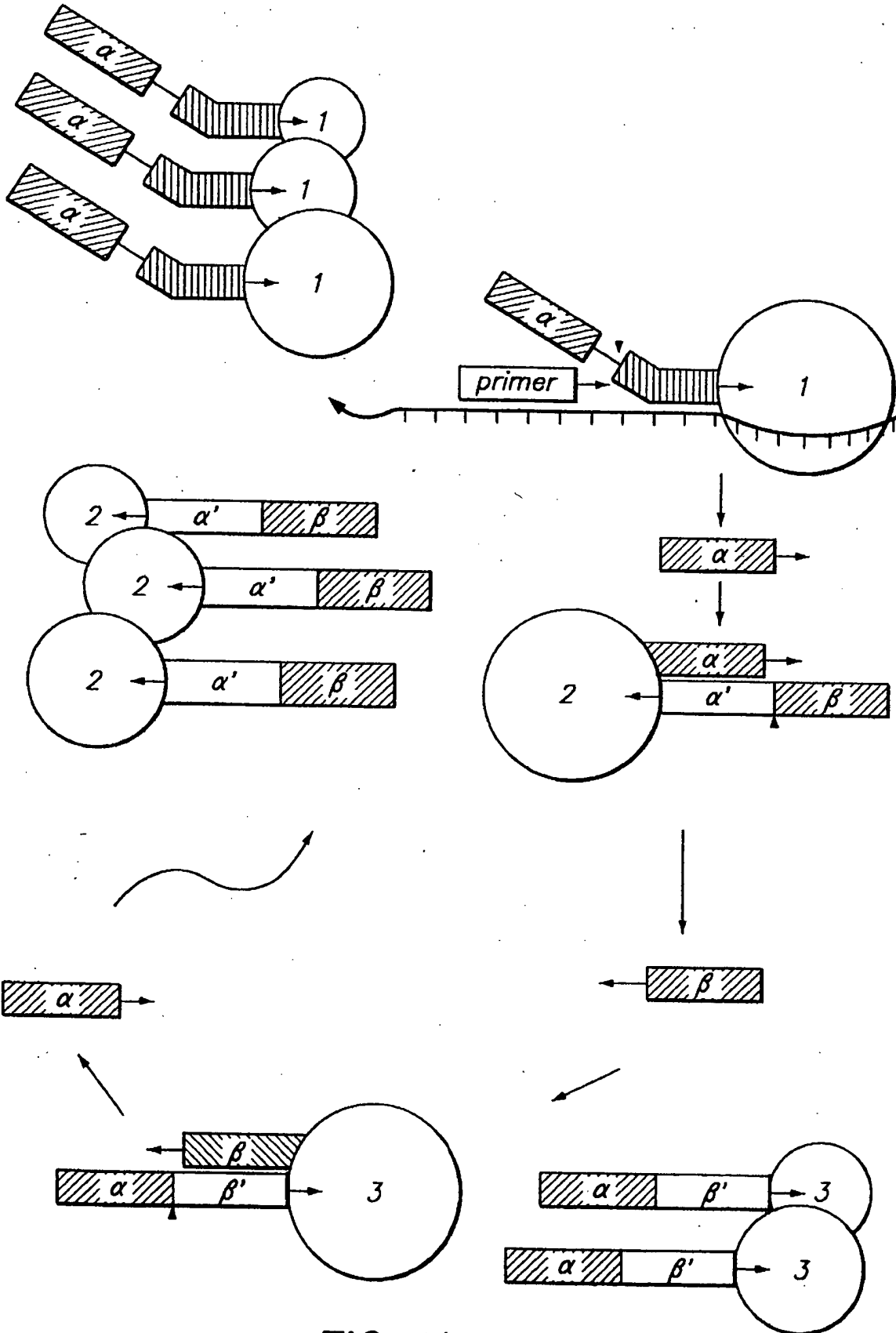
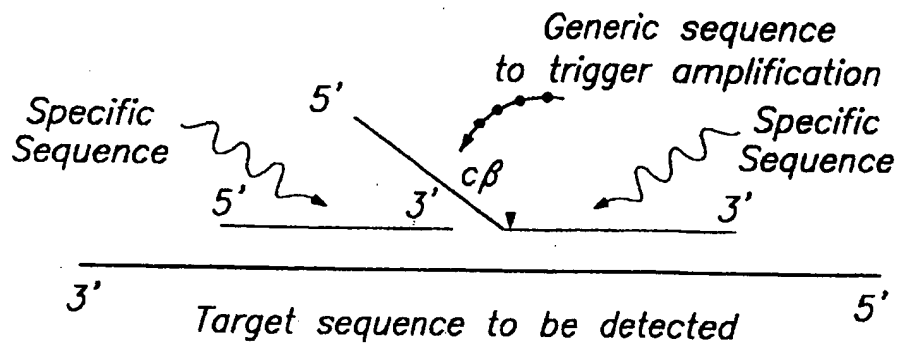


FIG. 1A



complement of  $\alpha$

5'  $c\beta$  3'

B-hairpin

3'

$c\beta$  5'

5'  $\alpha$

$c\beta$  3'

$\beta$  3'

A-hairpin

1 cut

Denature, anneal

First B-hairpin

3'

$c\alpha$

$\alpha$  3'

$c\beta$  5'

Cleaved A-hairpin

3'  $\beta$

Denature, anneal

Second molecule of A-hairpin

5'  $\alpha$

5'  $c\beta$  3'

$\beta$  3'

2 cuts

Cleaved B-hairpin

B-hairpins

3'

3'

4 cuts

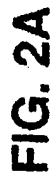
Cleaved A-hairpins

3'

3'

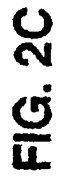
A-hairpins

**FIG. 1C** PART TWO: DETECTION REACTION



MAJORITY	[SEQ ID NO:7]	ATGXXGGGGATGCTTCCCGCTGTTGAGCCCAAGCCCGGCTCTCTGGTGGACGGCCACGACCTGGCCCT	70
DNAPTAO	[SEQ ID NO:1]	...AG..G.....G.....	70
DNAPTFL	[SEQ ID NO:2]	.....C..G.....	67
DNAPTTH	[SEQ ID NO:3]	...GA.....G.....A.....	70
MAJORITY		ACGGCACCTTCTTCGGCCCTGAAGGGCTCAGCACCGCCGGGGGGAACGGGTGCAGGGCGGTCTACGGCTT	
DNAPTAO		.....CA.....G.....	140
DNAPTFL		.....T.....C.....C..T.....	137
DNAPTTH		.....G.....	140
MAJORITY		CGCCAAAGAGGGCTCCTCAAGGGCCCTGAAGGAGGACCGGGACXXGGGGGTGXTGGTGGTCTTTGACGGCCAAG	
DNAPTAO		.....C.....A.....	207
DNAPTFL		...A.....GT..T.....	204
DNAPTTH		.....T..AA..C..CT.....	210
MAJORITY		GGCCCGCTCCTTCGGCCACGAGGGCTACGAGGGCTACAAGGGCGGGCGGGCCCCCAGGAGGACCTTC	
DNAPTAO		.....G..GG.....G.....	277
DNAPTFL		.....	274
DNAPTTH		.....GA.....G.....C.....C.....	280
MAJORITY		CGGGGAGGCTCGGGCTCATCAGGAGGCTGGTGGACCTCCTGGGGCTTGGCGGGCTCGAGGTCGGCGGGCTA	
DNAPTAO		.....A.....T.....G.....G.....	347
DNAPTFL		.....G.....T.....A..C.....T..G..G.....T.....	344
DNAPTTH		.....T..A.C.....T..A.C.....	350

**FIG. 2B**



ONAPIAQ	G.	C.	C.	G.	T.	A.	A.	C.	C.	1044
DNAPTFL	T.	CC.	GT.	T.	A.	C.	G.	G.	T.	1041
ONAPIIH	TG.	C.	G.	G.	G.	G.	CC.	G.	A.	1050



FIG. 2D

MAJORITY [SEQ ID NO:7]		CGGGGXCTCCTGGCGAAGGACCTGGCGGTTTTGGCCCTGAGGAGGGCCCTXGACCTCTTGGCCGGGGGAGG	
DNAPTAQ [SEQ ID NO:1]	.....G..T.....A.....AG.....C.....A.....T..G.....CC.....C.....	1114	
DNAPTFL [SEQ ID NO:2]	.....AA.....G.....G.....C.....C.....G.....T..C.....A..A.....	1111	
DNAPTTH [SEQ ID NO:3]	.....C.....C.....C.....TC.....G..A.....G.....G.....	1120	
MAJORITY		ACCCCATGGTGGCTAGCTCCTGGACCCCTCGAACACACGACCCCGGAGGGGGTGGCCCGGGCTACGG	
DNAPTAQ	.....T.....	1184	
DNAPTFL	.....G.....T.....T.....T.....	1181	
DNAPTTH	.....G.....G.....	1190	
MAJORITY		GGGGGAGTGGACGGAGGAXGGGGGGAGCGGGCGCTGGTCTTGGAGAGGGCTCTTCCXGAACCTXXGGGAG	
DNAPTAQ	C.....G.....G.....GC.....T.....GGC.....GTG..G..	1254	
DNAPTFL	.....T.....A.....GG.....C.C.....A..C.....AAA.....	1251	
DNAPTTH	.....C..C.CCG.C.....C..G.....CAT..G.....CCTTA..	1260	
MAJORITY		CGCCTTGAAGGGGAGGAGGGCTCCTTTGGCTTACGAGAGGTGGAGAGCCCTTTCCCGGGTCCCTGG	
DNAPTAQ	A..G.....A.....A.....A.....G.....G.....GGT.....	1324	
DNAPTFL	.....A.....A..A..AC.C..G.....G.....G.....GT.....	1321	
DNAPTTH	.....C.....A.....A.....C.....C.....A.....C.....	1330	
MAJORITY		CCGACATGGAGCGGACGGGGGTXCGGCTGGAGCTGGCCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGGA	
DNAPTAQ	.....G..C.....T.....AG.....T..G.....C.....	1394	
DNAPTFL	GG.....C.....C.....C.....A..G.....A..G.....	1391	
DNAPTTH	.....C.....A.....T.....T.....C.T.....	1400	



FIG. 2E

MAJORITY [SEQ ID NO:7] GGAGATCCGGCGCCCTCGAGGAGGAGGCTCTTCCGGCTGGCGCGCCACCCCTTCAACCTCAACTCGCGGGGAC		
DNAPTAQ [SEQ ID NO:1]	.....GC.....CC.....	1464
DNAPTFL [SEQ ID NO:2]	.....G.G.....AG..G.....	1461
DNAPTTH [SEQ ID NO:3]	.....T.....G.....	1470
MAJORITY CAGCTGGAAAGGGTGCCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAGACXGGCAAGC		
DNAPTAQ	.....C.....A.....	1534
DNAPTFL	.....GC.....G.C.G..T.....	1531
DNAPTTH	.....TA.....T.G.G..C.A.....	1540
MAJORITY GCTCCAGCAGCGCGCCGTGCTGGAGGGCCCTXCGXGAGGGCCACCCCATCGTGGAGAGATCCTGCAGTA		
DNAPTAQ	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CGGC.....	1601
DNAPTTH	.....G.....A..G.....C..C..C..	1610
MAJORITY CGGGGAGCTCAGCAAGCTCAAGAACAGGTAGATXGACCGCCCTGCCXGXCCTCGTCCAGCCGAGGACGGGC		
DNAPTAQ	.....G.....G.....T.....T.....G.A..A.....	1674
DNAPTFL	.....A.....A.....C.C..G.....A..C..	1671
DNAPTTH	.....G.G.....C..AAG.....G.....	1680
MAJORITY CGGCTGCACAGCCGGCTTCAACGAGAGCGGCCACGGCCAGGGGAGGCTTAGTAGCTCCGAGCCCAACCTGC		
DNAPTAQ	.....A.....T.....C..	1744
DNAPTFL	.....G.....C.....TCC.....	1741
DNAPTTH	.....G.....	1750





FIG. 2F

MAJORITY [SEQ ID NO:7] AGAACATCCCCGTCCGACGCCXCTG66CCAGAGGATCGCGCGGGGCTTCGT66CCGAGGAGG6GT66GT  
DNAPTAQ .....G..T..G.....A..C.....G...C.. 1814  
DNAPTFL .....G.....T.....C..C.....A.....C..... 1811  
DNAPTTH .....CT.....G.....G.....T.....G 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCGGGGTCTTGGCCCGACCTCTCGGGGAGGAGAACCTG  
DNAPTAQ A.....T..T.....C.....A.....G.....C..... 1884  
DNAPTFL .....T..T.....C.....T.....T.....C..... 1881  
DNAPTTH .....T..T.....C.....G.....A..... 1890

MAJORITY ATCCGGGCTTCCAGAGGGGAGGAGATCCACAGCCAGAGCGGCGAGCTGGATGTTGGCGCTCCCCCGG  
DNAPTAQ .....G.....G.....G.....G.....G.....G... 1954  
DNAPTFL .....T.....T.....T.....T.....T.....C.. 1951  
DNAPTTH .....A.....A.....A.....A.....A..... 1960

MAJORITY AGCGCGTGGACCCCTGATCGCGCGGGCGGCGGCAAGACCATCAACTTCGGGGTCTCTAGCGGCA18TCCGG  
DNAPTAQ .....A..G..A.....T.....G.....G.....G... 2024  
DNAPTFL .....A..G..A.....T.....G.....G.....G... 2021  
DNAPTTH .....A..G..A.....T.....G.....G.....G... 2030

MAJORITY CCACCGCCTCTCCGAGGAGCTTGGCATCCGCTAGGAGGAGGCGGTGGCTTTCATTGAGCGCTACTTCCAG  
DNAPTAQ .....A.....T.....CCA.....T... 2094  
DNAPTFL .....GG.....T.....T.....T... 2091  
DNAPTTH .....TA..G.....T.....T.....A 2100



FIG. 2G

MAJORITY [SEQ ID NO:7] AGCTTCCCAAGGTGGGGCCTGGATTGAGAAACACCTGGAGGAGGGCGGGGTACGTGGAGA

DNAPTAQ [SEQ ID NO:1] ..... 2164  
DNAPTFL [SEQ ID NO:2] ..... 2161  
DNAPTTH [SEQ ID NO:3] ..... 2170

MAJORITY CCTCTTGGGGCCGGGGCCTACGTGCCCGAGCTCAAGGGCCGGGTGAAGAGCGGTGGGGGAGGGGGCGGGA

DNAPTAQ ..... 2234  
DNAPTFL ..... 2231  
DNAPTTH ..... 2240

MAJORITY GCGCATGGCCTTCAACATGCCCGTCCAGGGCCAGCCGCGGACCTCATGAAGTGGCCATGGTGAAGCTC

DNAPTAQ ..... 2304  
DNAPTFL ..... 2301  
DNAPTTH ..... 2310

MAJORITY TTCCCCCGGCTXCAGGAAATGGGGCCAGGATGCTGCTXCAGGTCACAGGAGGAGCTGGTCTCGAGGGCCC

DNAPTAQ ..... 2374  
DNAPTFL ..... 2371  
DNAPTTH ..... 2380

MAJORITY CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTTGGCCAAAGAGGTGTCATGGAGGGGGTCTATCCCTGGCCGT

DNAPTAQ ..... 2444  
DNAPTFL ..... 2441  
DNAPTTH ..... 2450



FIG. 2H

MAJORITY [SEQ ID NO:7]	CCCCCTGGAGGTGGAGGTGGGATGGGGAGGACTGGCTCTCGGCCCAAGGAGTAG
DNAPTAA [SEQ ID NO:1]	.....A.....GA
DNAPTFL [SEQ ID NO:2]	.....CC.....
DNAPTTH [SEQ ID NO:3]	.....T.....GT...



FIG. 3A

MAJORITY [SEQ ID NO: 8] MXAML PLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLLKALKEDG-DAVXUVFDAK

TAQ PRO	[SEQ ID NO: 4]	RG	H	69
TFL PRO	[SEQ ID NO: 5]			68
TTM PRO	[SEQ ID NO: 6]	E	YK.F	70

MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPQYEADDVLATLAKKAEKEGYEVRI L

TAQ PRO	GG	A	S	139
TFL PRO		V	F	138
TTM PRO		FT	R	140

MAJORITY TADRDLYQLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPQVKGIGECTAXKLLX

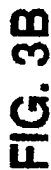
TAQ PRO	K	H	D	A	T	E	R	E	209	
TFL PRO		E	I	Y	A	I	QR	IR	208	
TTM PRO		V	V	H	E	F	V	L	K	210

MAJORITY EWGSLENLLKNLDRVKP-XXREKIXAHMEDLXLSXLSXVRTDLPLEVDFAXRREPDRGIRAFLERLF

TAQ PRO	A	L	AI	L	D	K	WD	AK	K	R	278
TFL PRO		FOH	Q	SL	LG	A	A	RK	Q	H	277
TTM PRO			ENV	K	L	R	LE	R	L	QG	280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAELLALAAARXGRVHRAXDPLXGLRDLKEV

TAQ PRO	S				K	D	G	PE	YKA	A	348
TFL PRO		G	A		L	SF	G	WE	L	Q	347
TTM PRO		A	AP				K	C	D	A	350



..	E	R	O	698
..	S	G	G	697
..	K	V		700



FIG. 3C

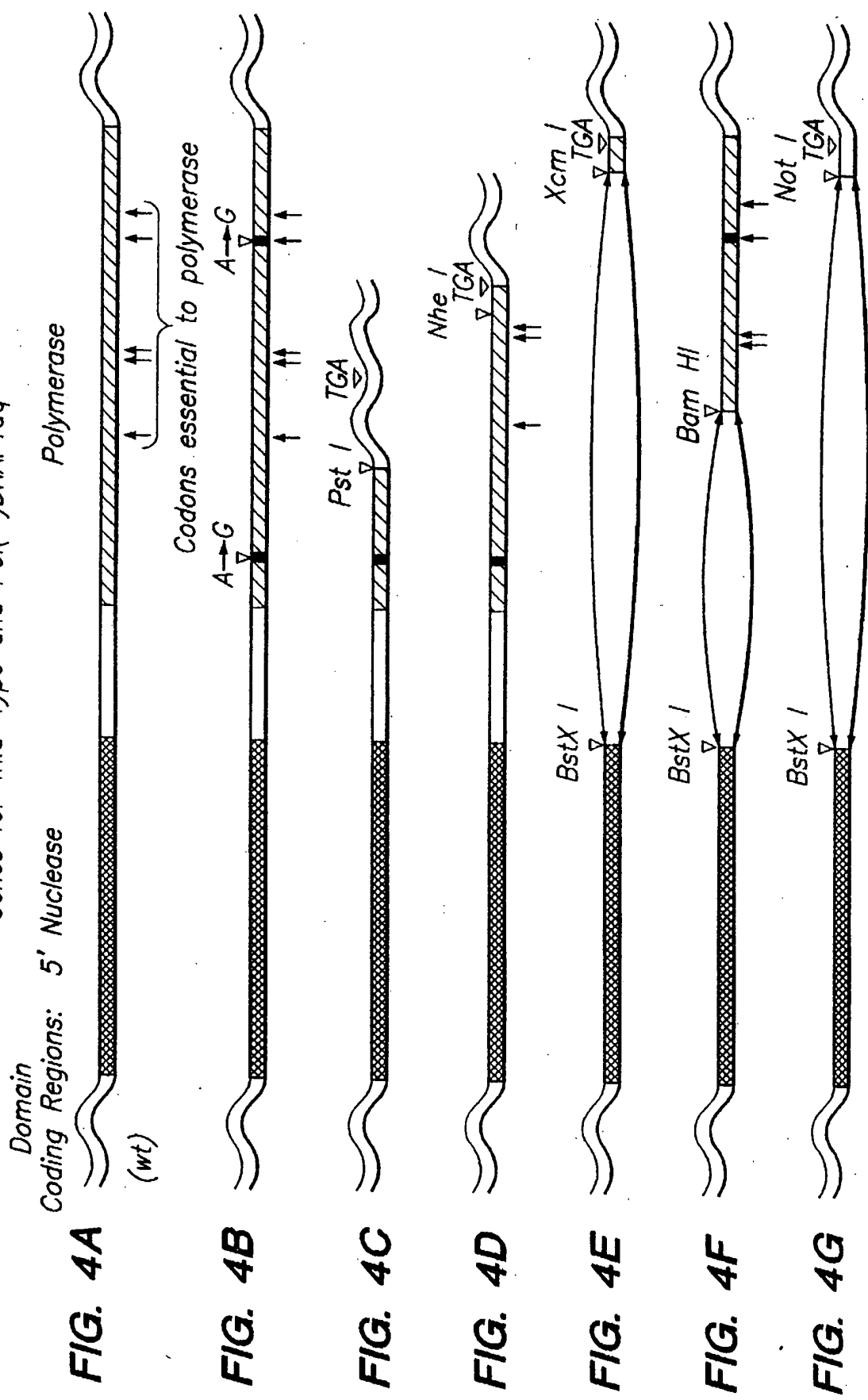
MAJORITY [SEQ ID NO: 8] SFPKVRAWIEKTL ECGRRRGYVETLFGRRRYVPDLNARVKSUREAERMAFNMPVQGTADLMKLA MVKL

TAQ PRO [SEQ ID NO: 4]	.....E.....	768
TFL PRO [SEQ ID NO: 5]	.....G.....R.	767
TTH PRO [SEQ ID NO: 6]	.....K.....	770

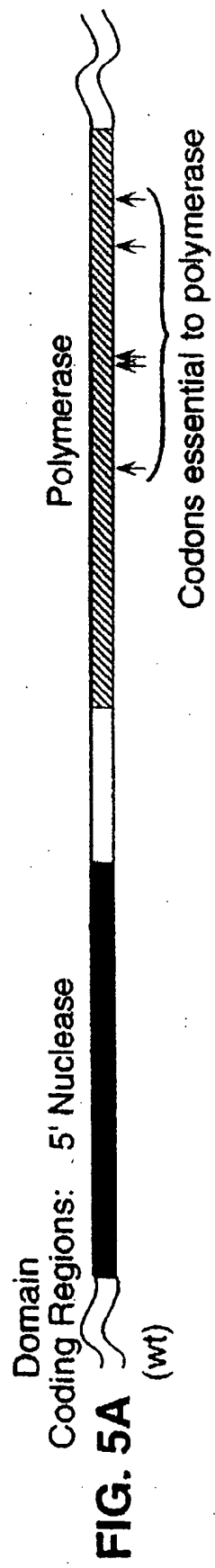
MAJORITY FPRLEXMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAQ PRO	.....E.....E...A...R.....I.....	833
TFL PRO	.....Q.L.....D...R.....W..O.....L.....	831
TTH PRO	.....R.....L.....QA...E.....A..KA.....M.....G	835

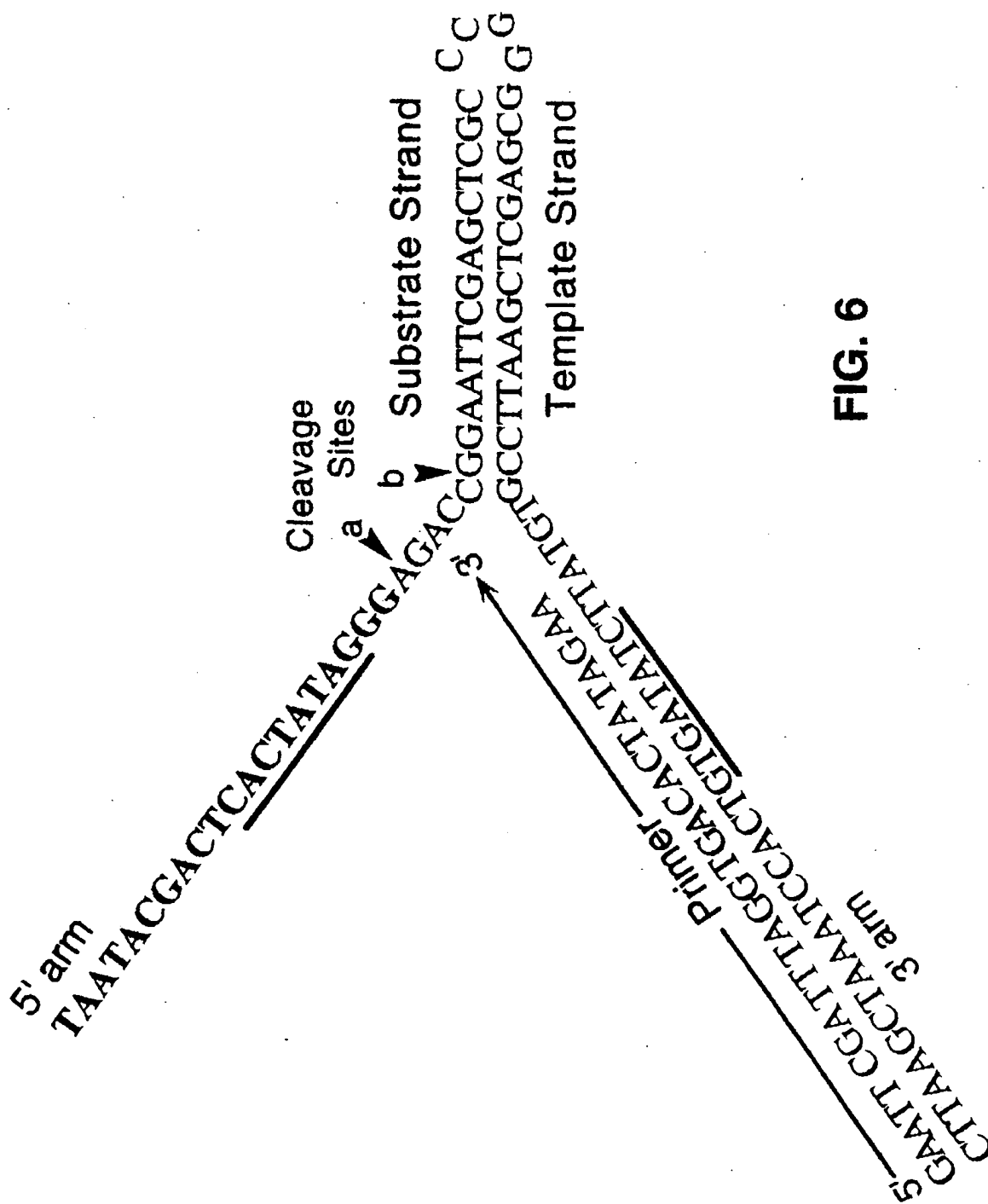
Genes for Wild-Type and Pol(-)DNAPTaq



Genes for Wild-Type and Pol(-) DNAPTfl







**FIG. 6**

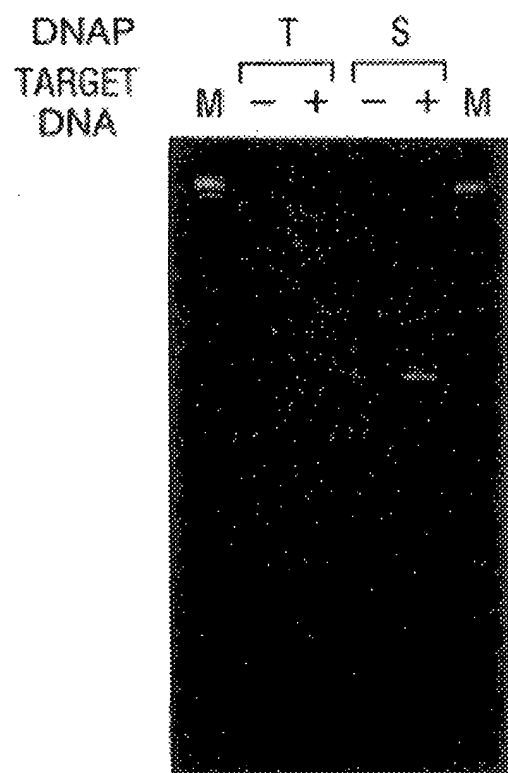


FIG. 7

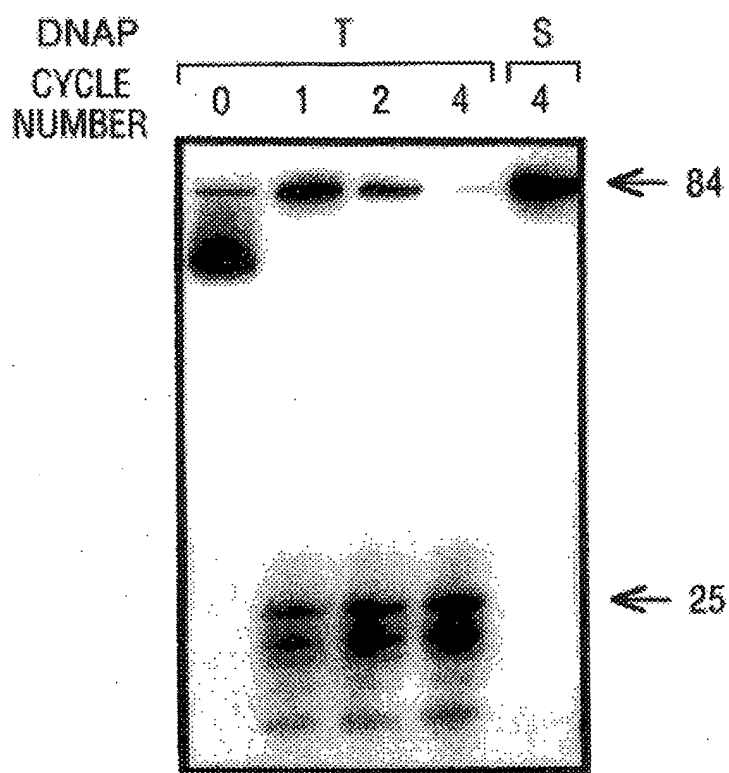


FIG. 8



	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

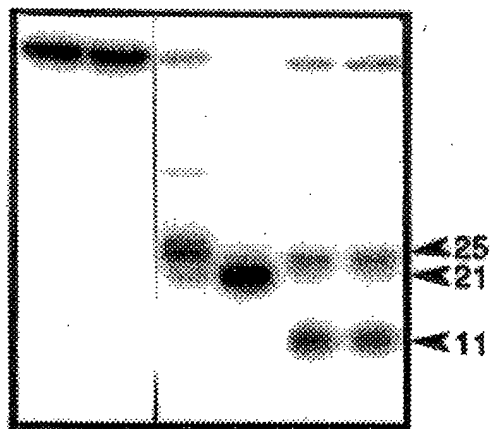


FIG. 9A

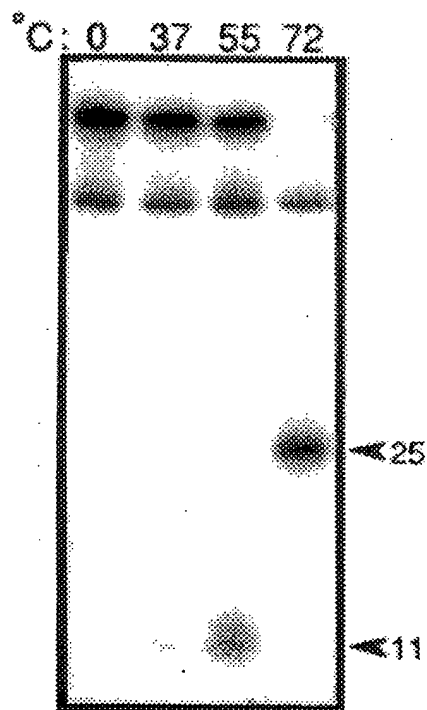


FIG. 9B

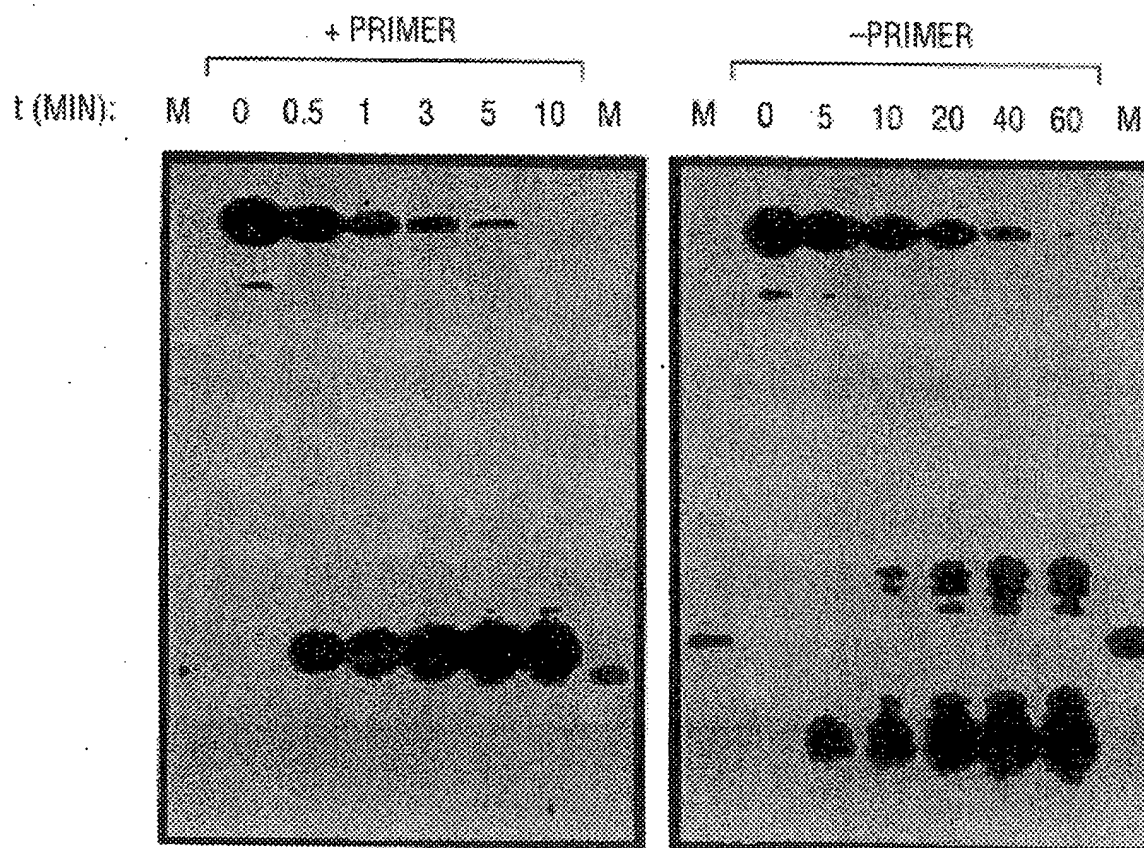


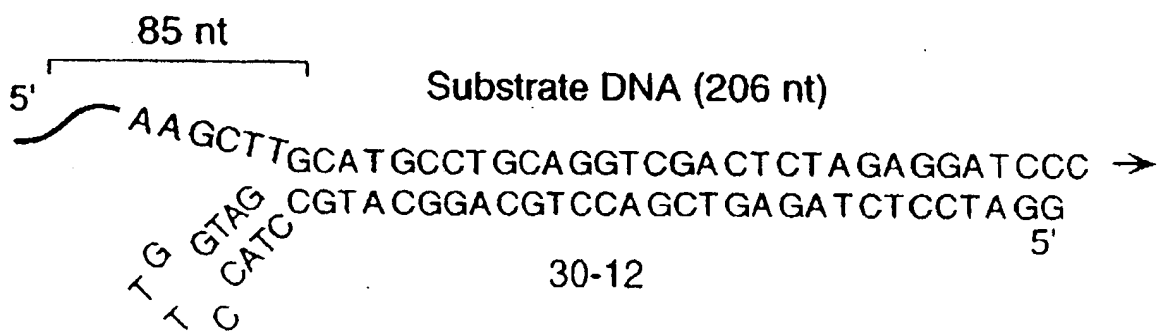
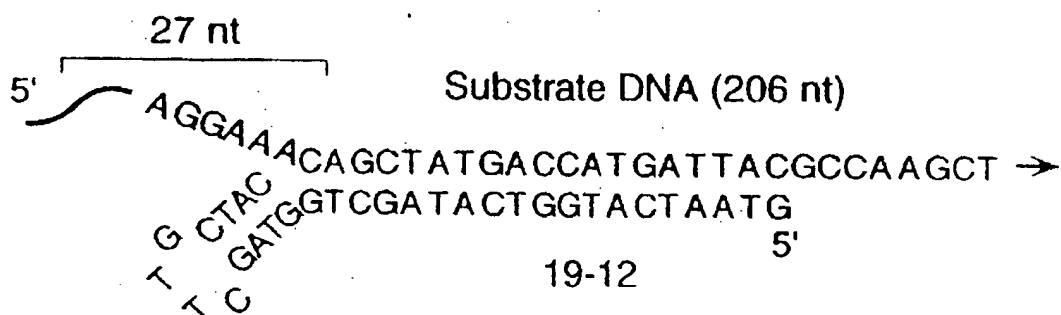
FIG. 10A

FIG. 10B





FIG. 12A



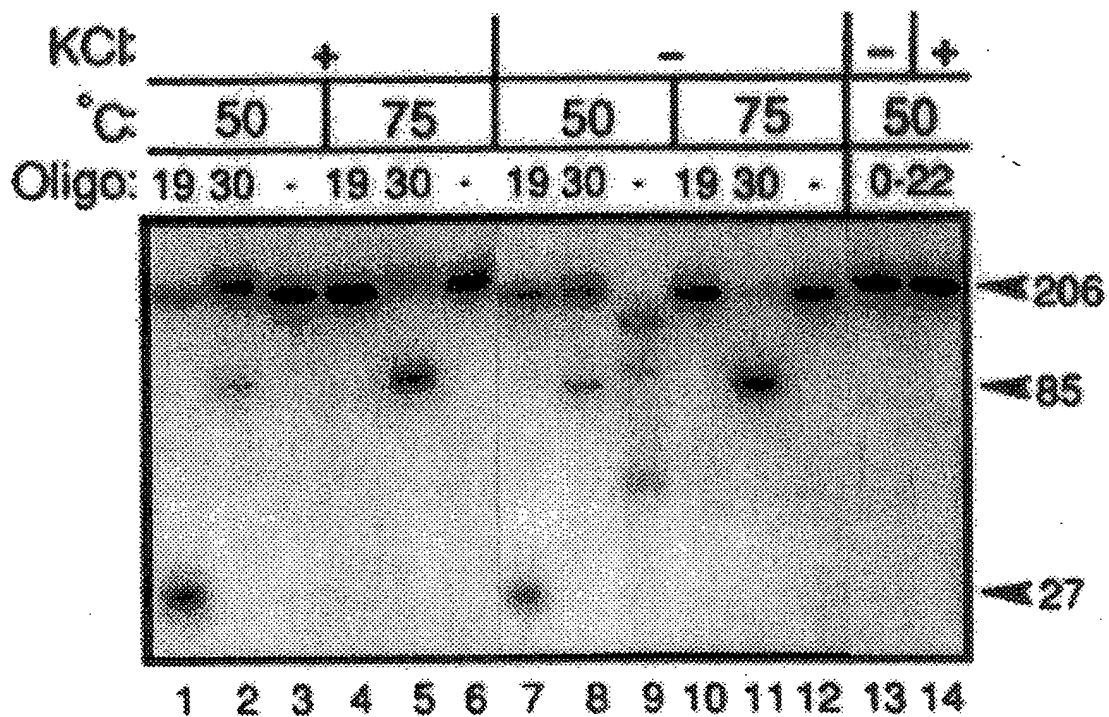


FIG. 12B

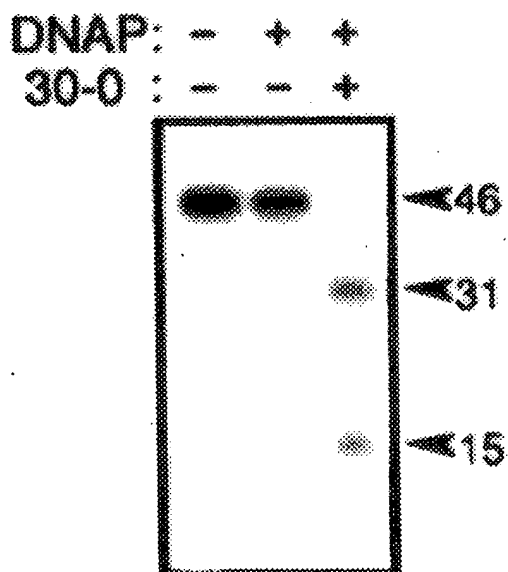
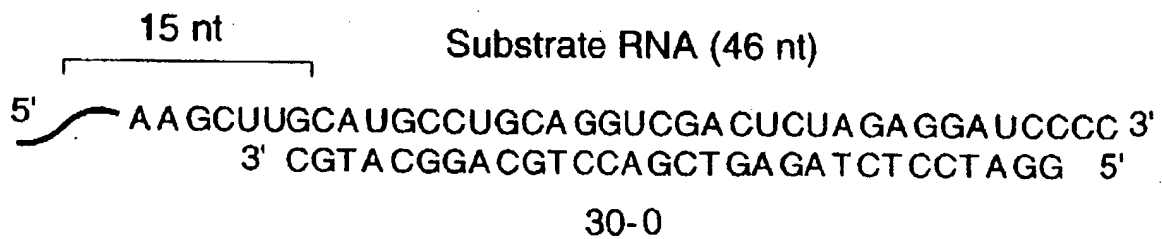


FIG. 13B





**FIG. 13A**

-35  
 TTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGGGGATAACAATTCACACAGGAACAGCG  
 -10  
 MetAsnSer...  
 ATGAATTTCGAGCTGGGTACCCGGGATCCTCTAGATCGACCTGCAGGCATGCAAGCTTGGCACTGGCC  
 EcoRI KpnI BamHI Sall XbaI PstI HindIII  
 SstI SmaI

FIG. 14B

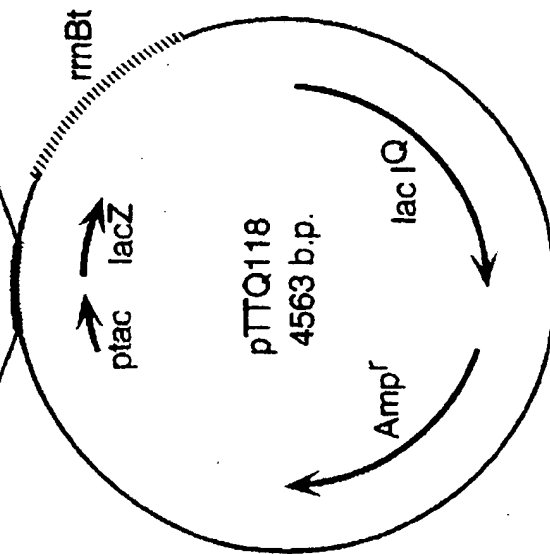
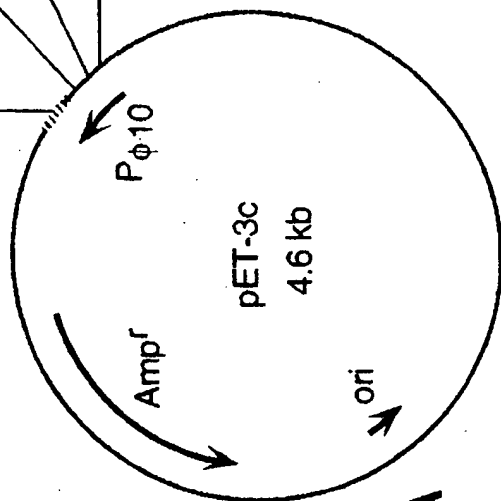
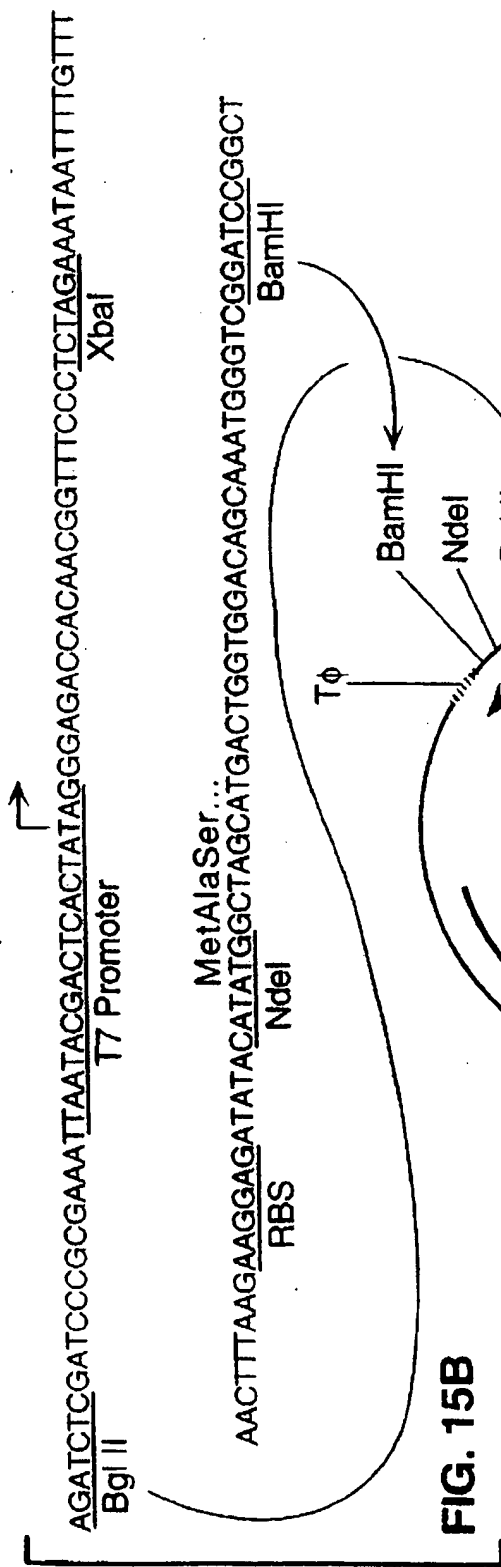


FIG. 14A

RBS: Ribosome binding site  
 ptac: Synthetic tac promoter  
 lac IQ: Lac repressor gene  
 lacZ: Beta-galactosidase alpha fragment  
 rmBt: E. coli rmB transcription terminator

FIG. 14C



P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter  
 Tφ: T7 φ Terminator  
 RBS: Ribosome binding site

**FIG. 15C**

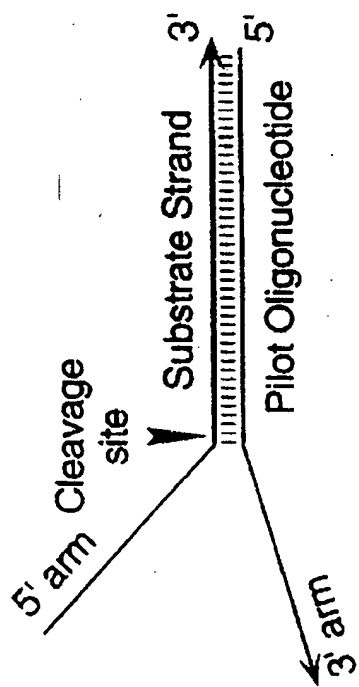


FIG. 16A

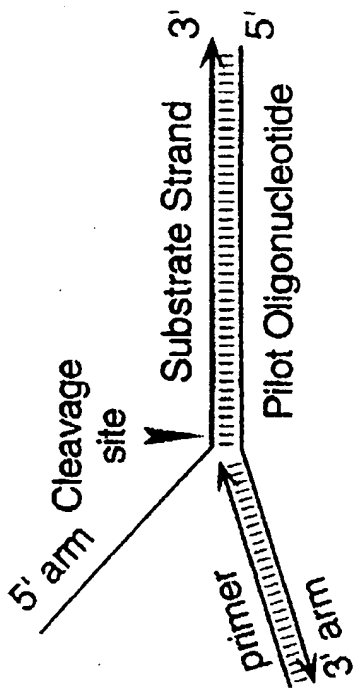


FIG. 16B

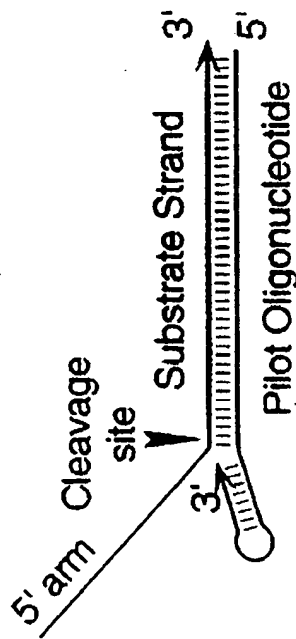


FIG. 16C

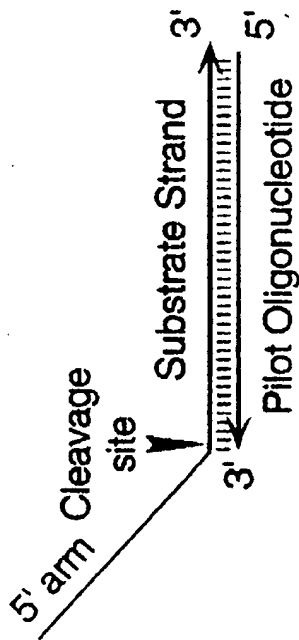


FIG. 16D

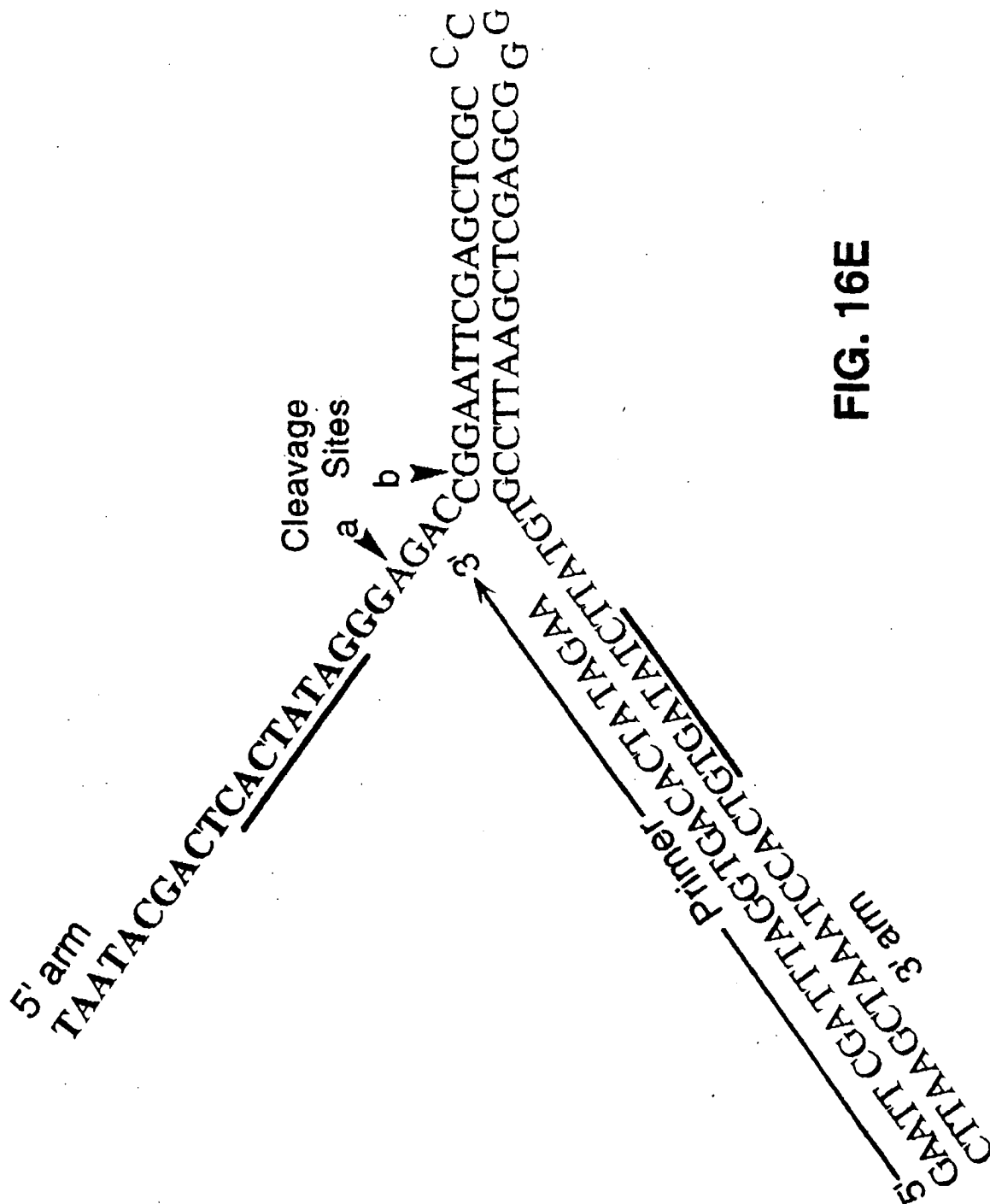


FIG. 16E

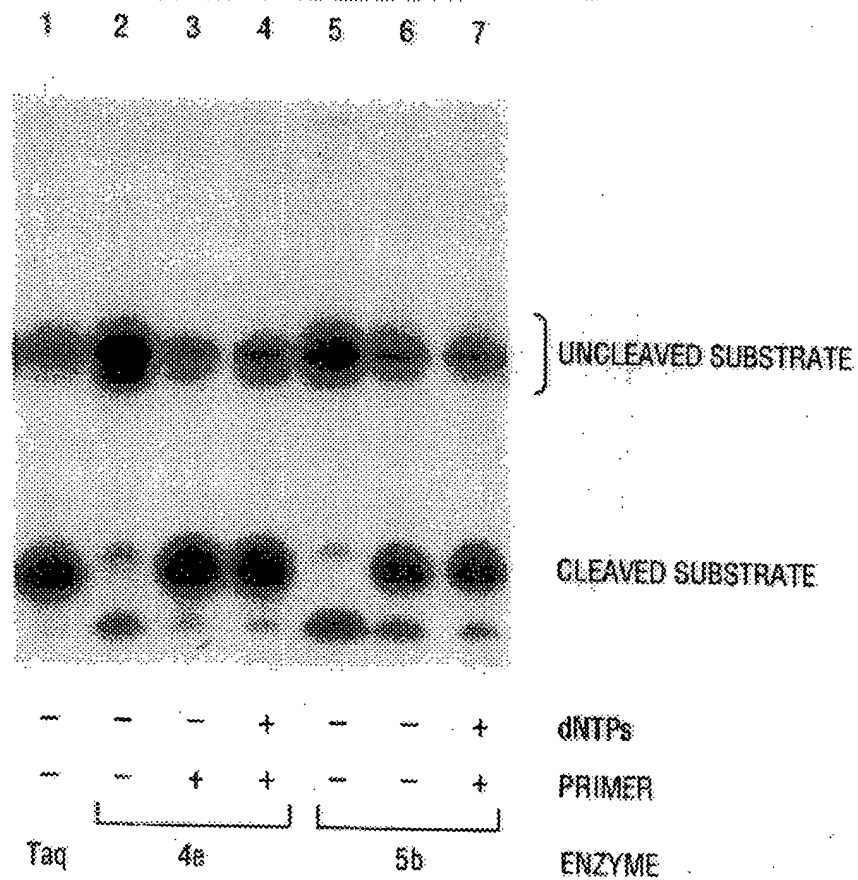


FIG. 17

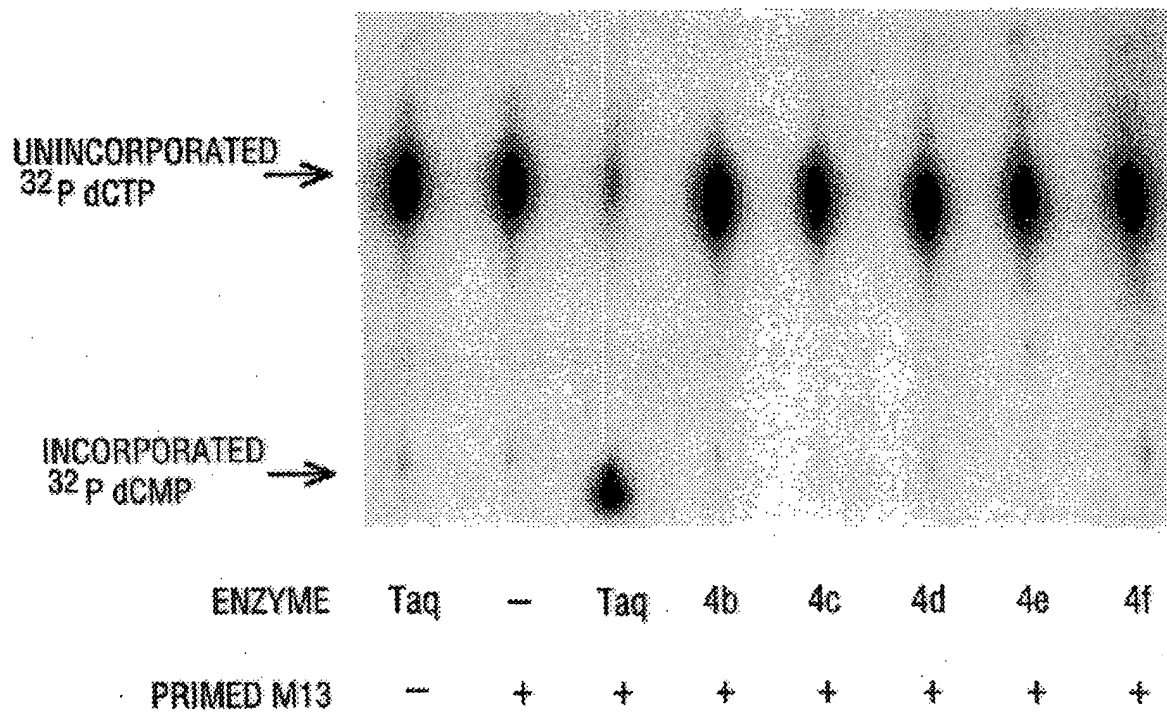


FIG. 18

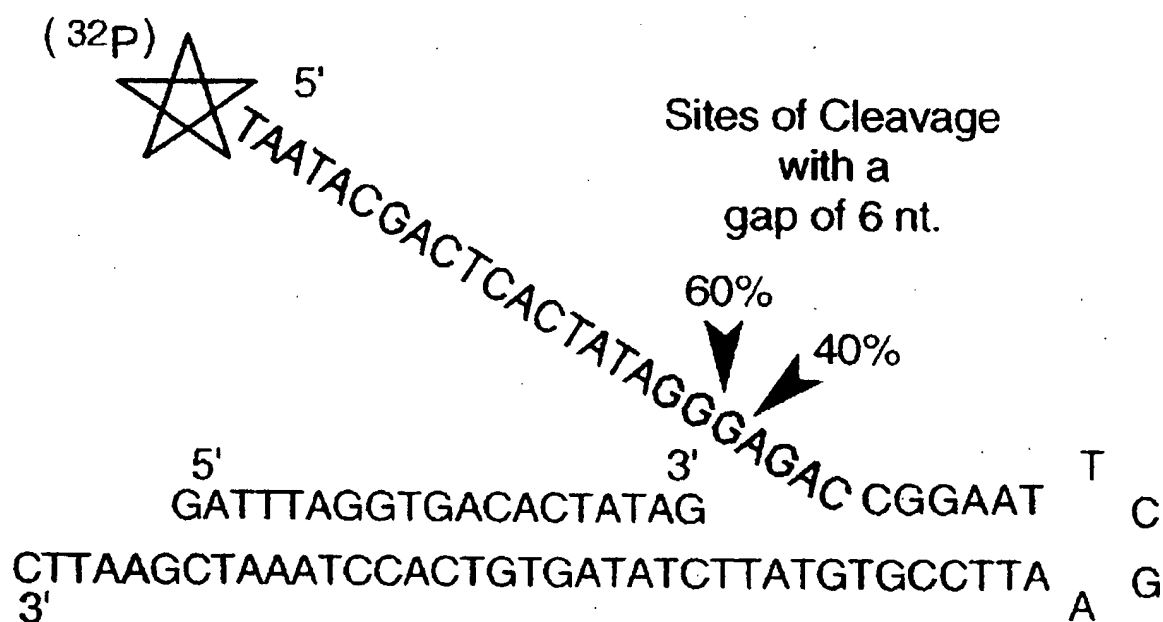
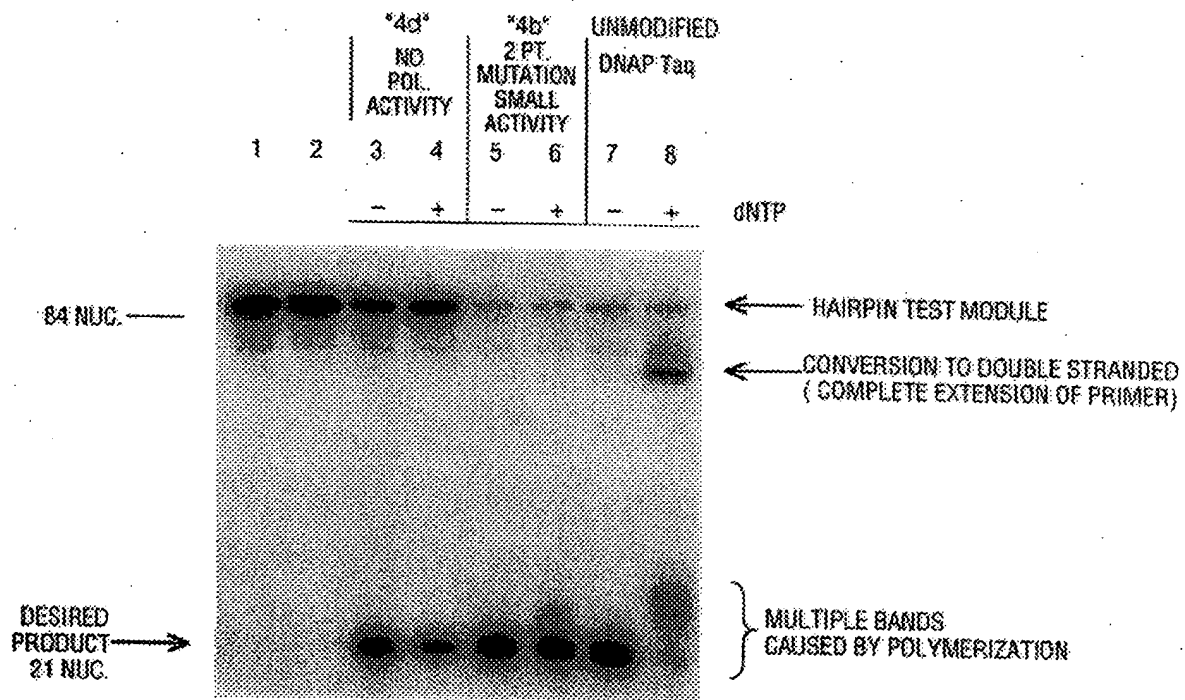


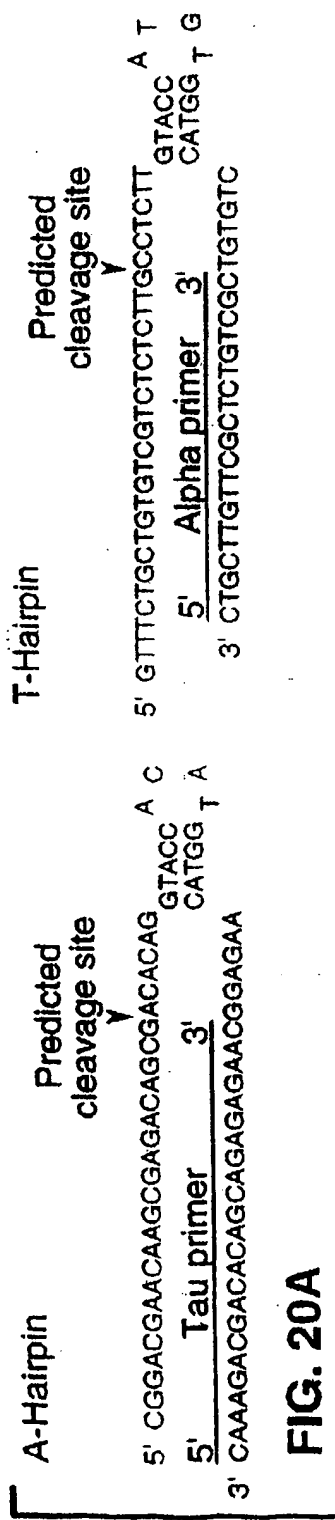
FIG. 19A





**FIG. 19B**

↑ SOME ABERRANT CLEAVAGE WITH \*4b\* BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

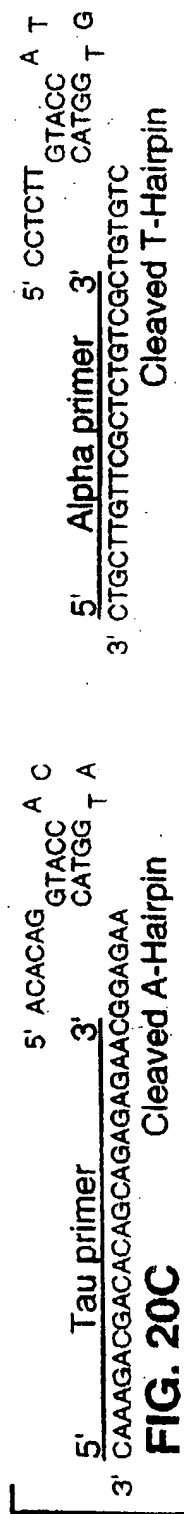


**FIG. 20A**

**Sequence of alpha primer:**

5' GACGAACAAGCGAGACAGCG 3'

**FIG. 20B**



**FIG. 20C**

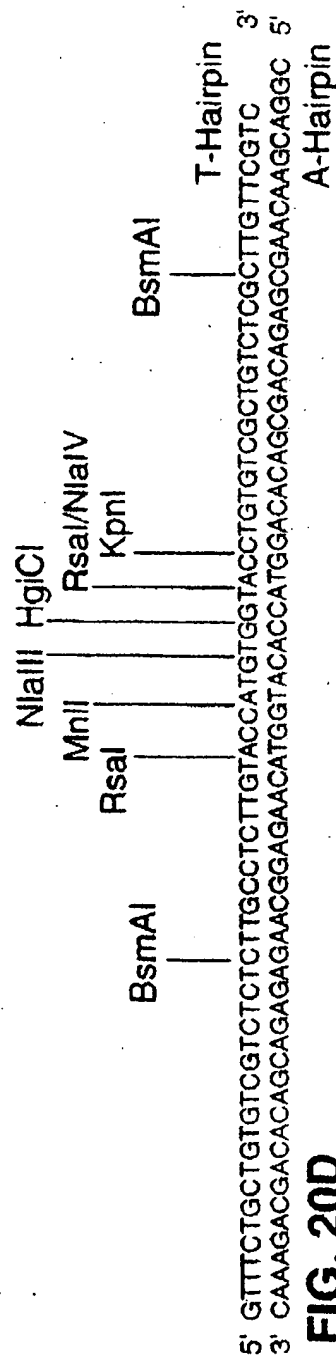


FIG. 20D

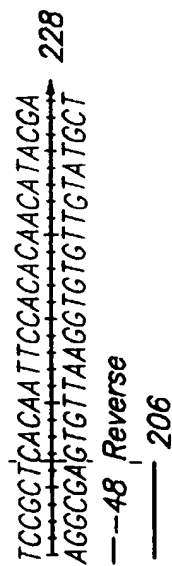
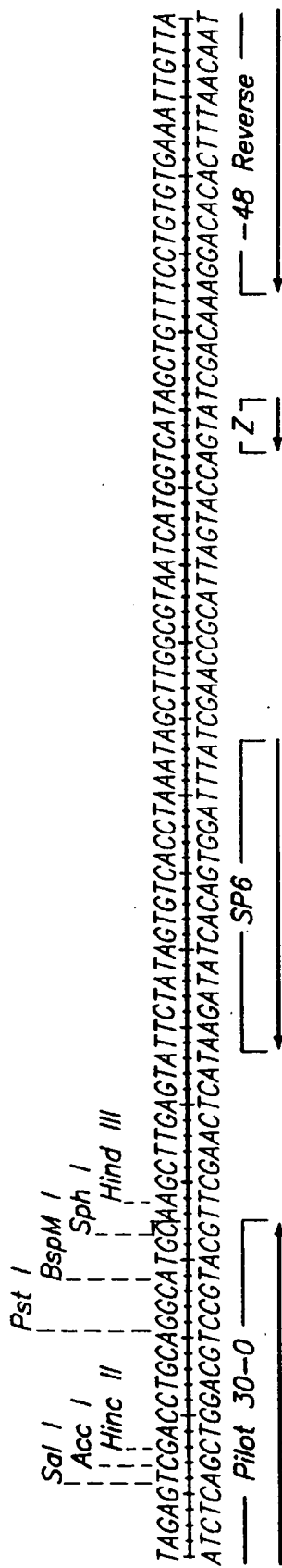
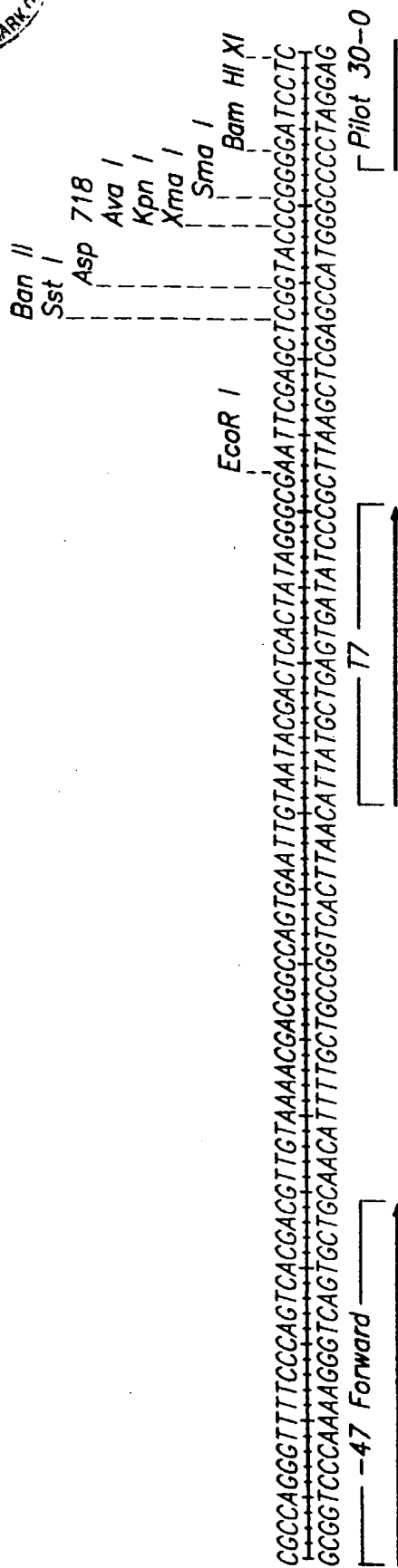
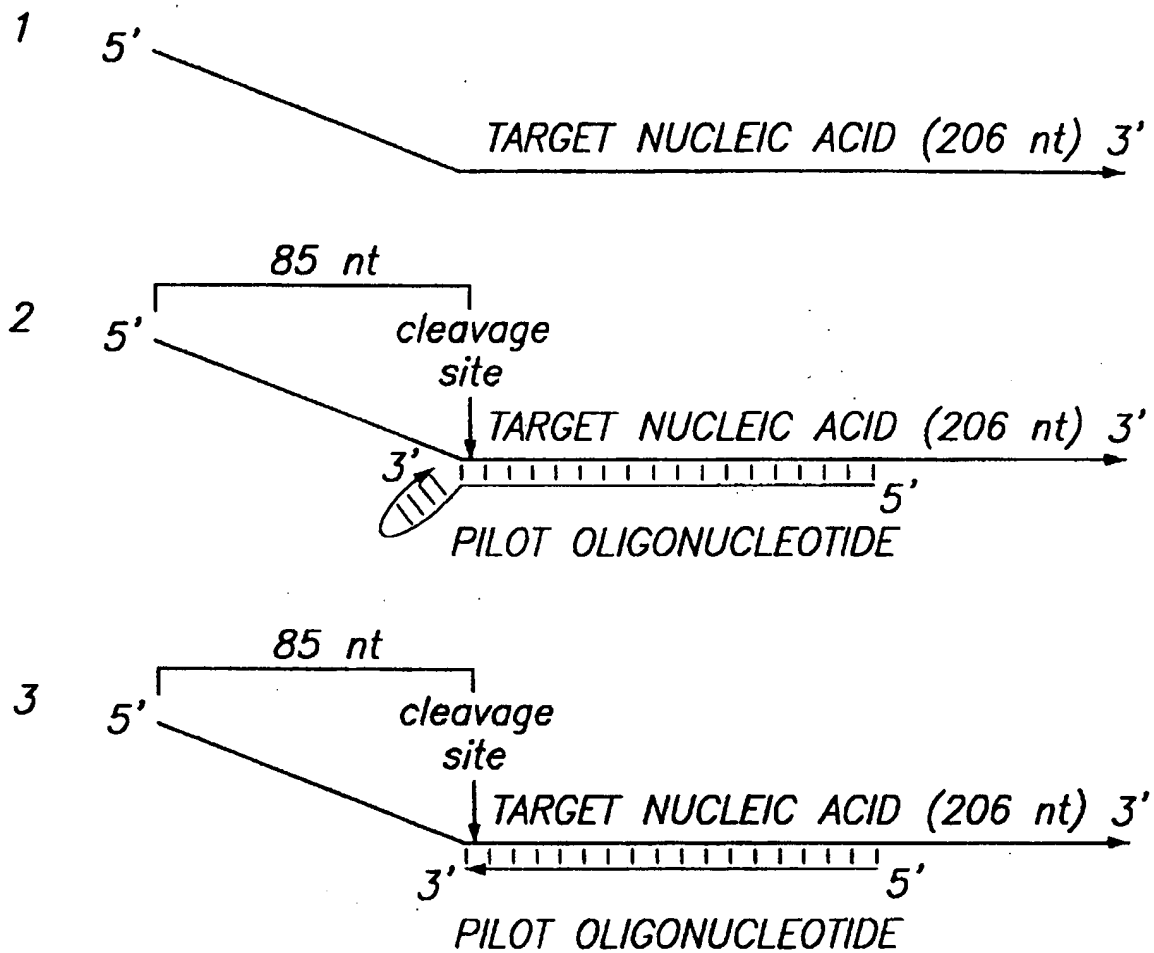


FIG. 21



**FIG. 22A**

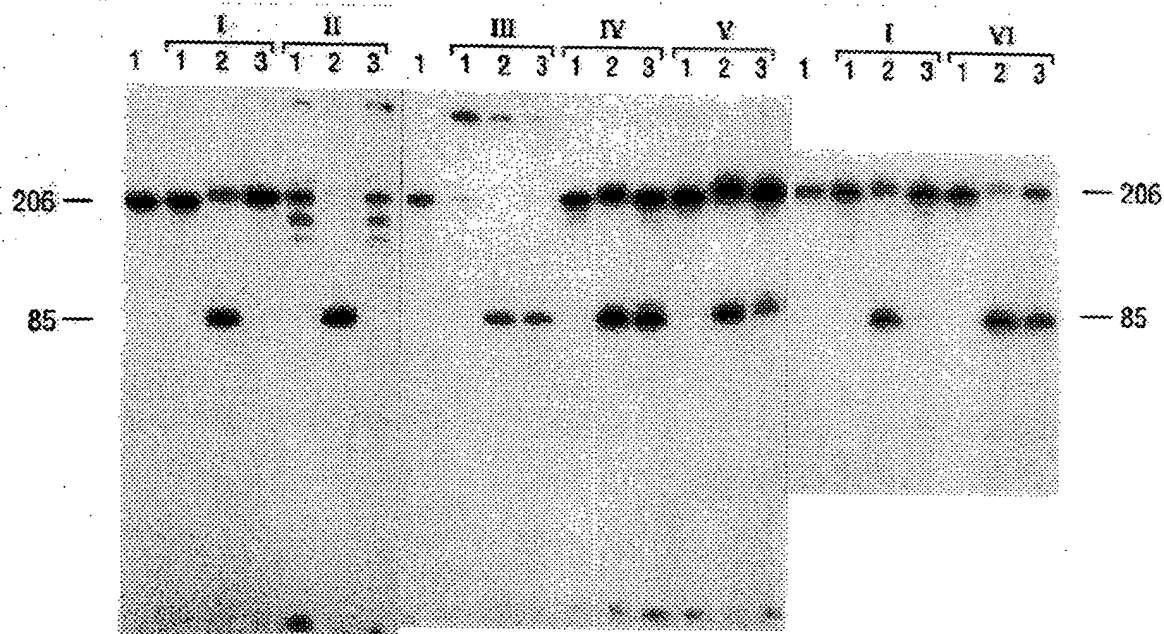


FIG. 22B

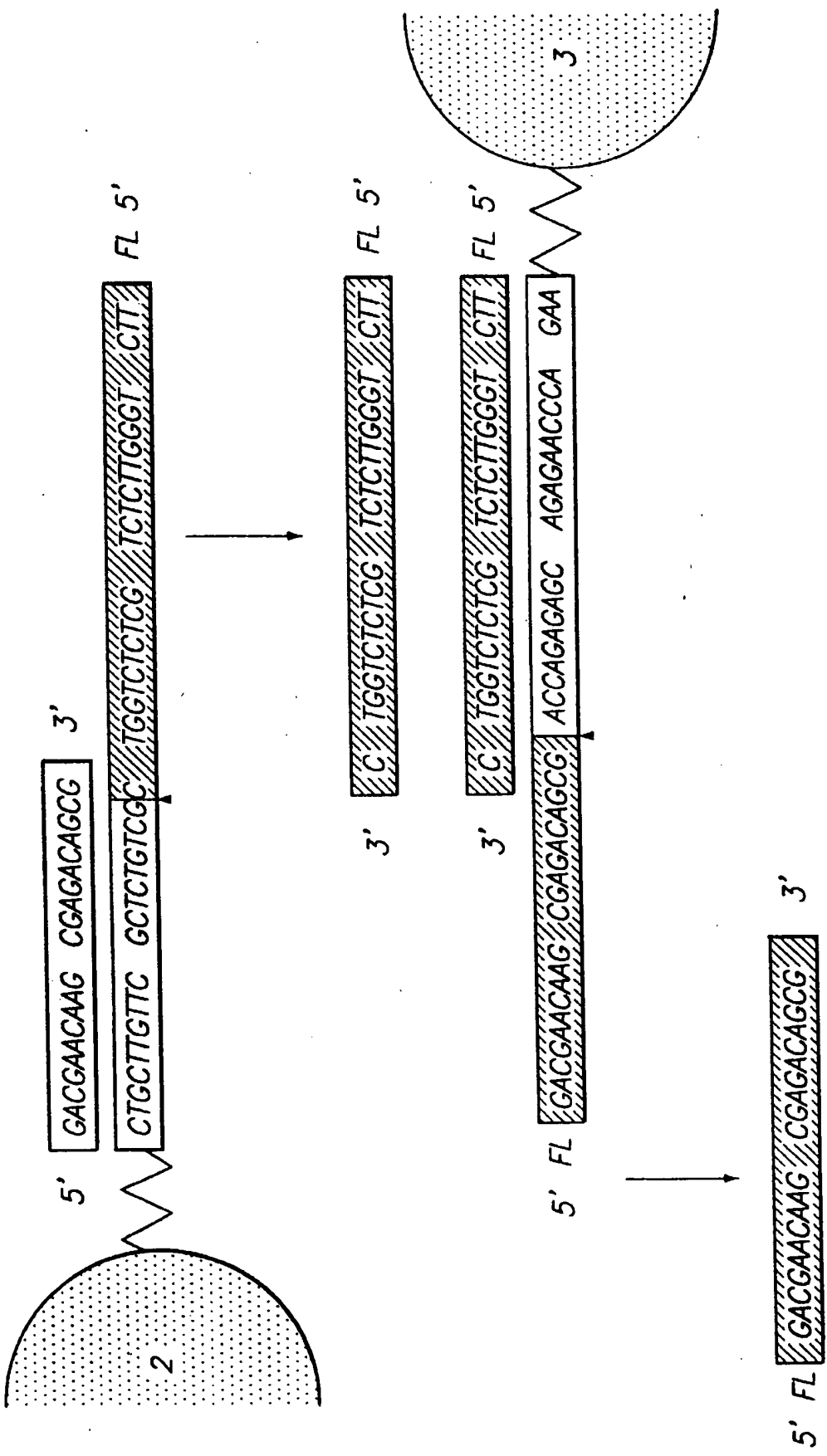


FIG. 23



CDR BEAD			T	T	T	A/T	A/T	A	A	A		
PILOT			-	-	+	-	+	+	-	-		
CLEAVASE	M	M	-	+	+	+	+	+	+	-	M	M

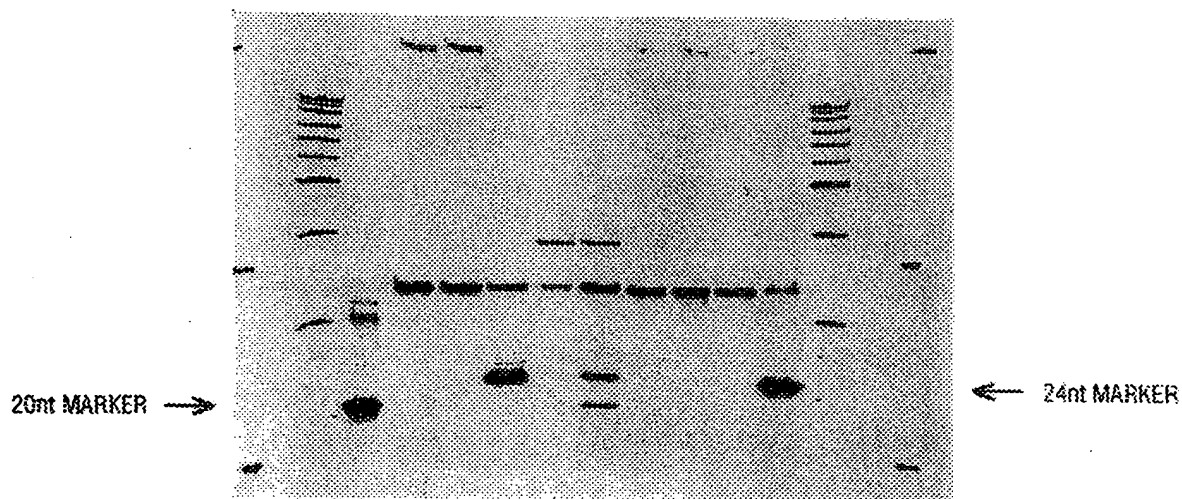


FIG. 24

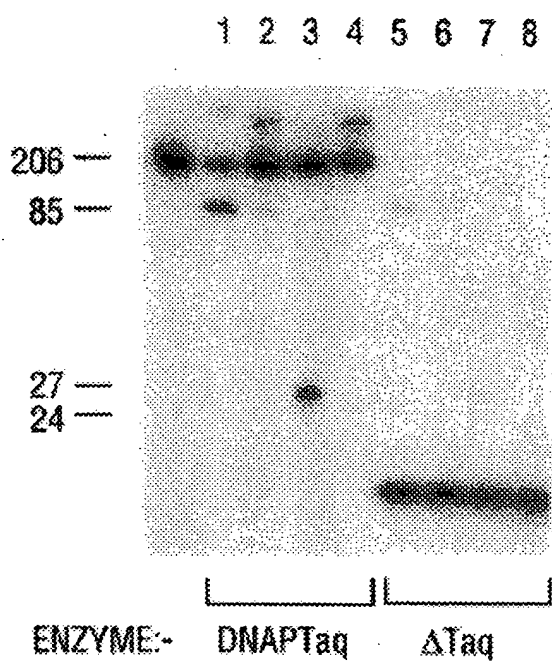


FIG. 25A

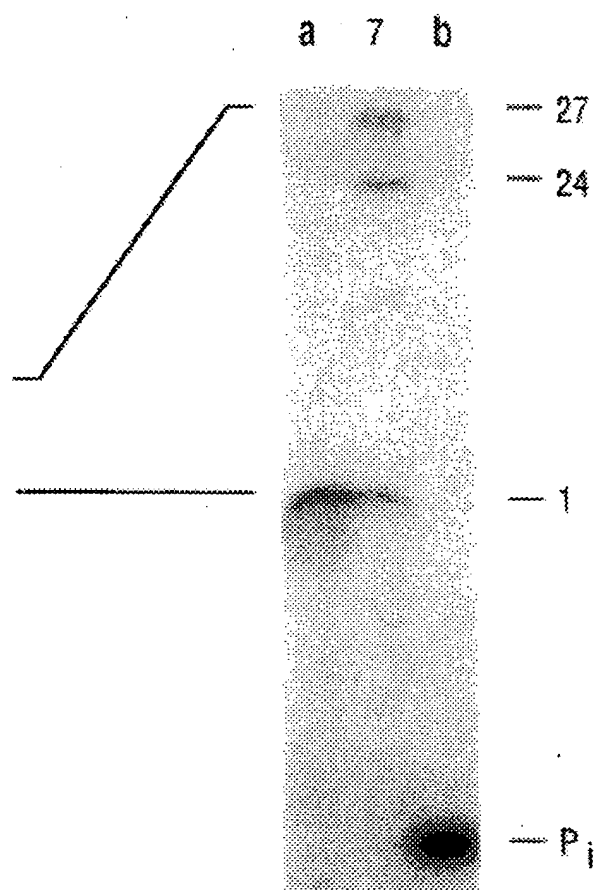


FIG. 25B





FIG. 26A

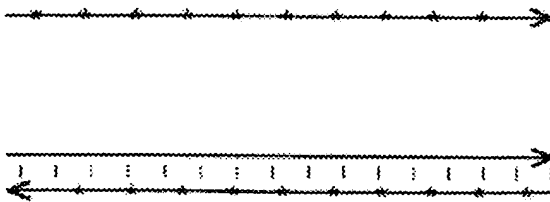
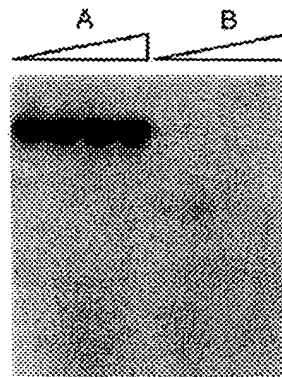


FIG. 26B

\* = 32p



— 206

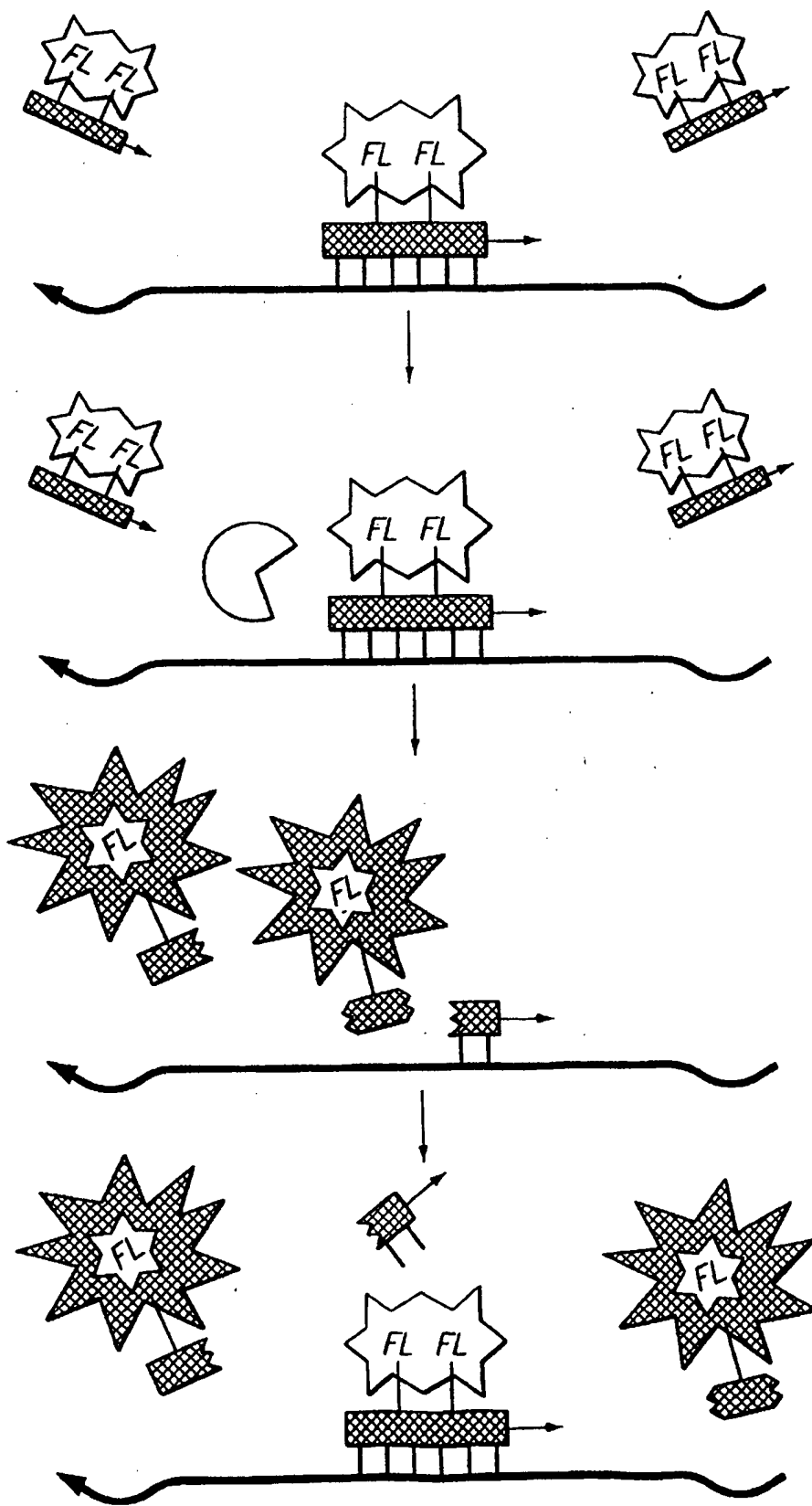
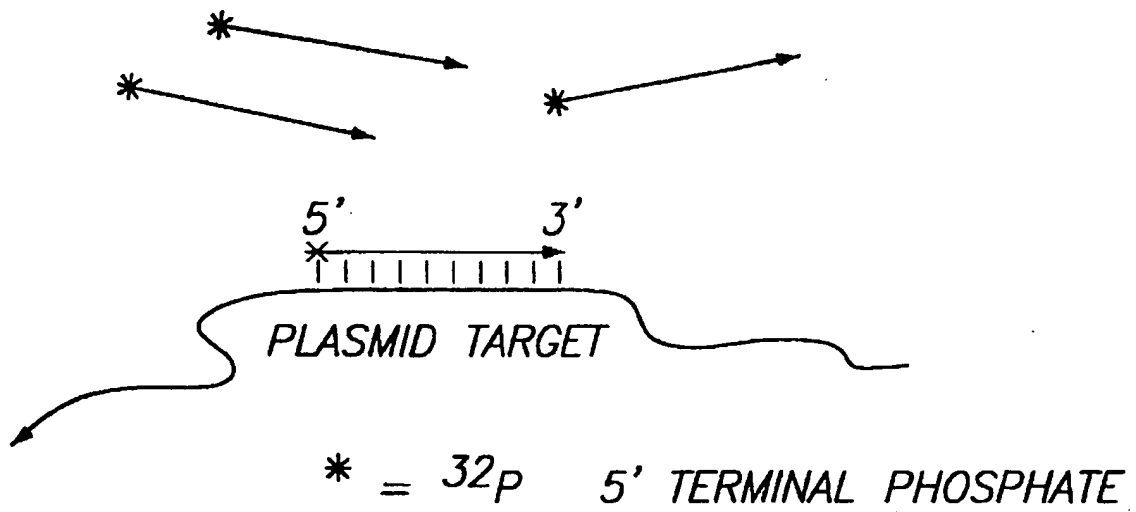
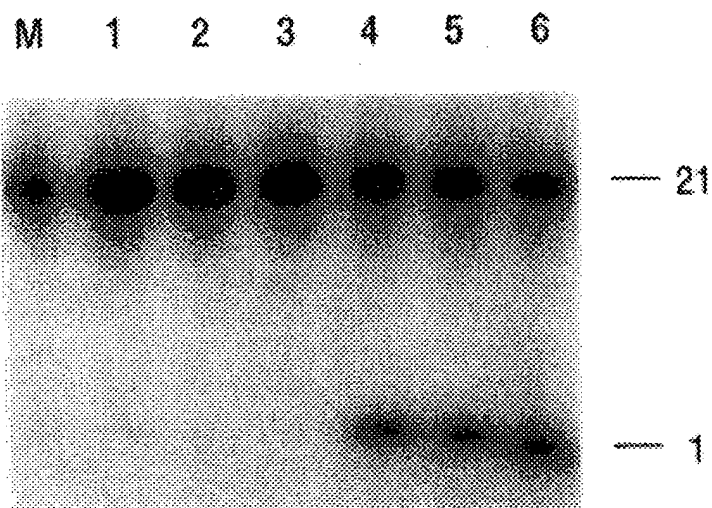


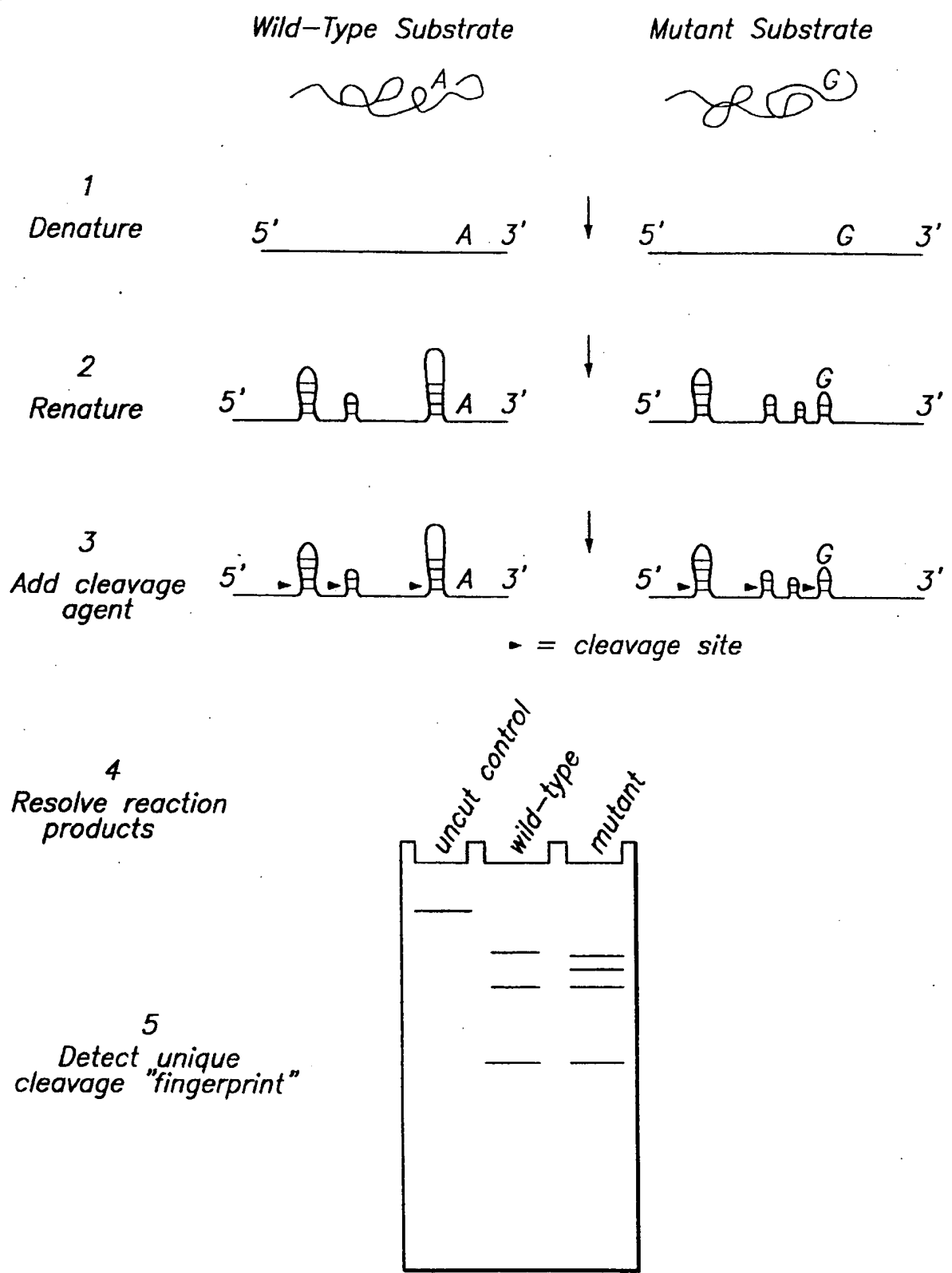
FIG. 27



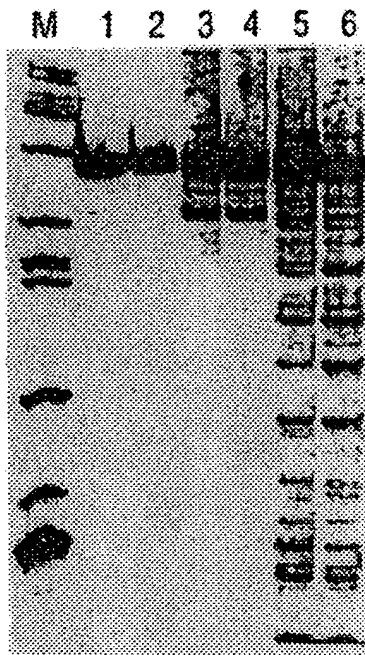
**FIG. 28A**



**FIG. 28B**



**FIG. 29**



**FIG. 30**

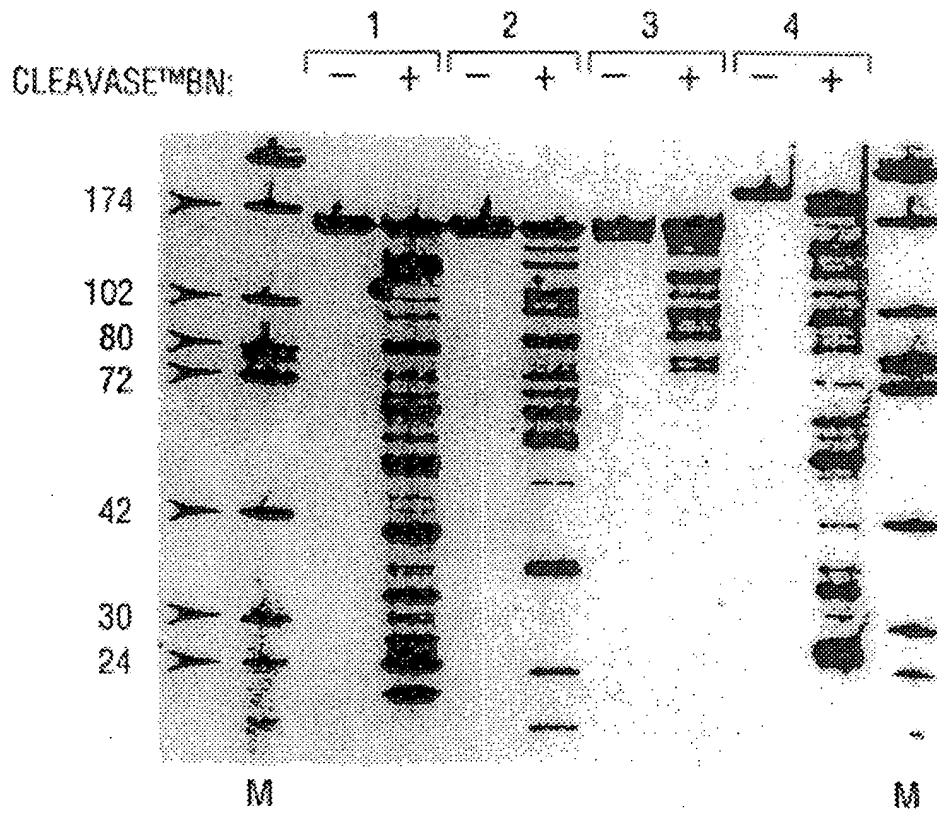


FIG. 31

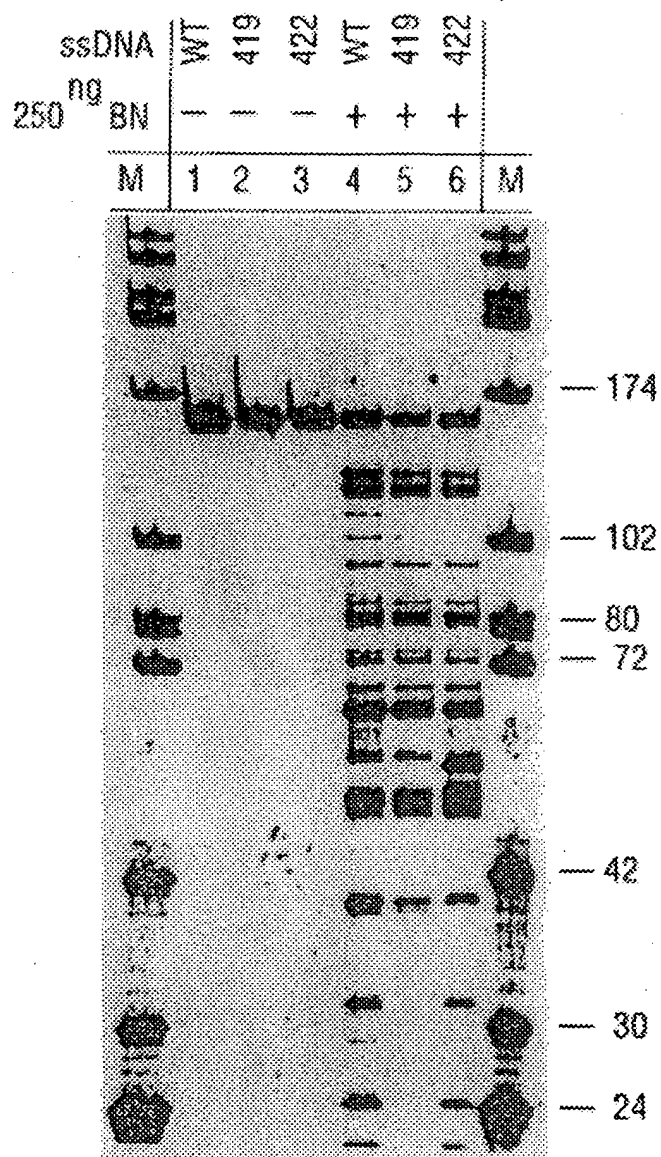


FIG. 32



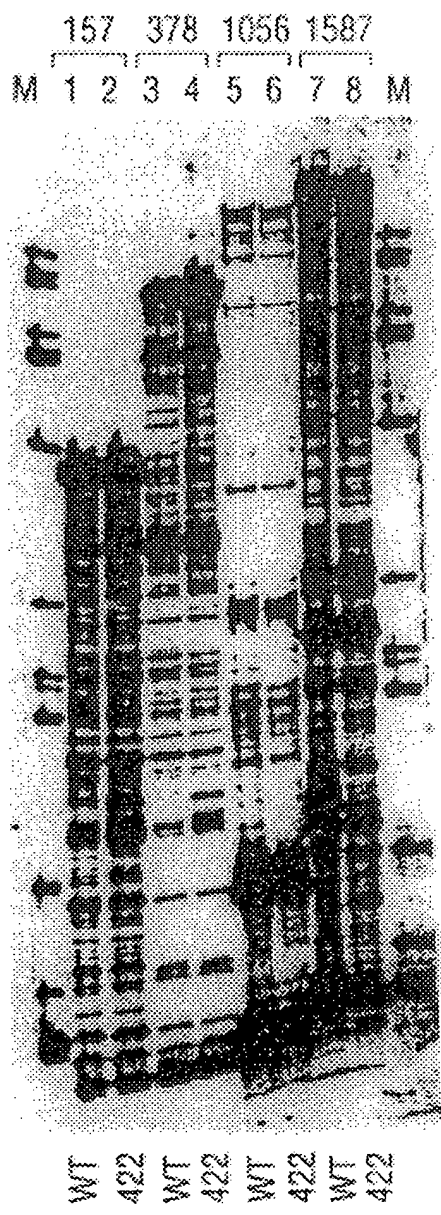


FIG. 33

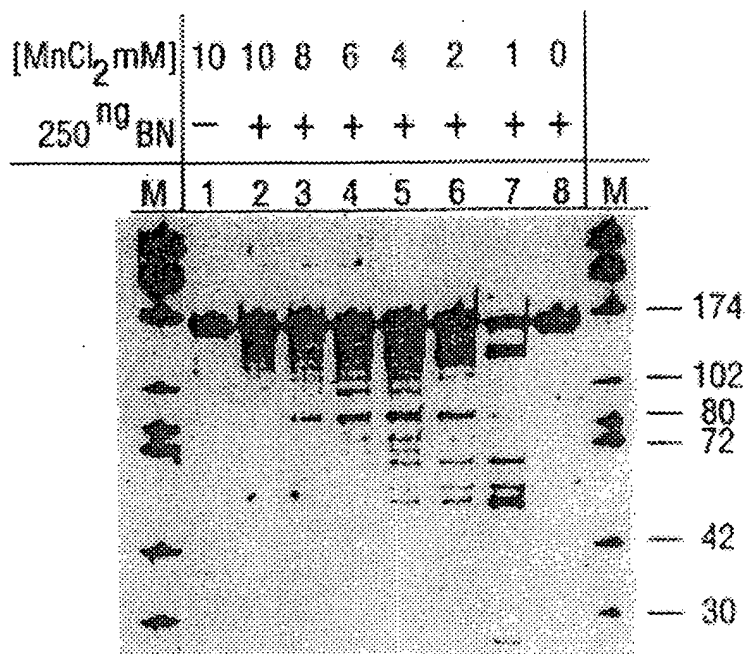


FIG. 34

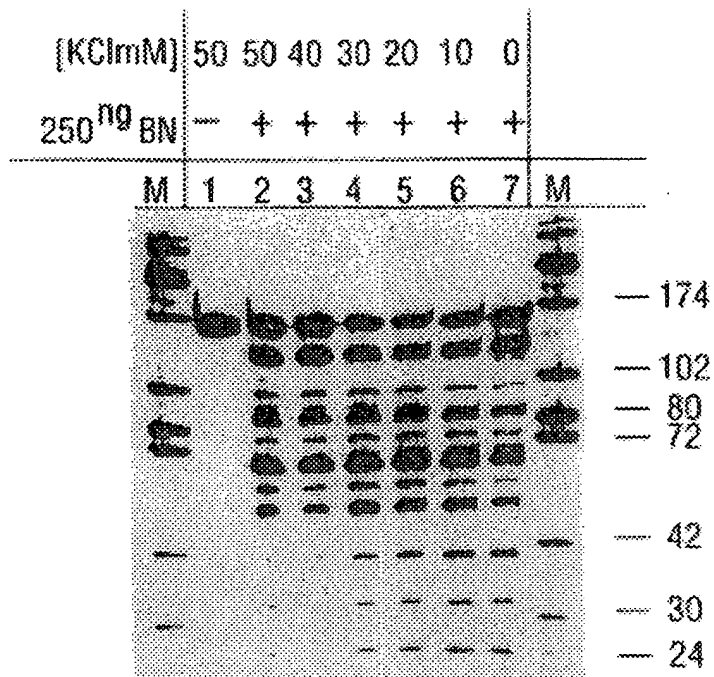


FIG. 35

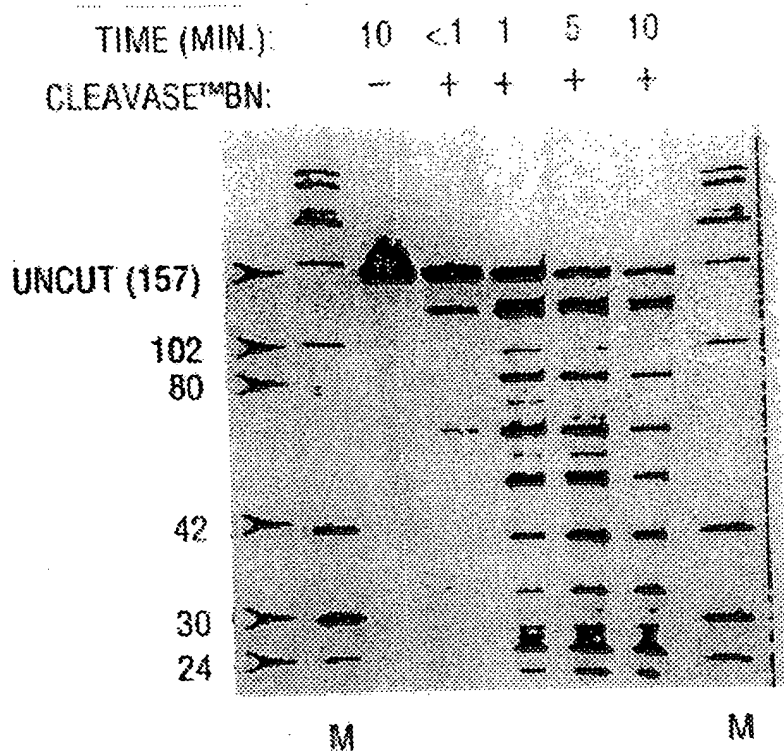


FIG. 36



TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	-	-	+	+	+	+	-	+

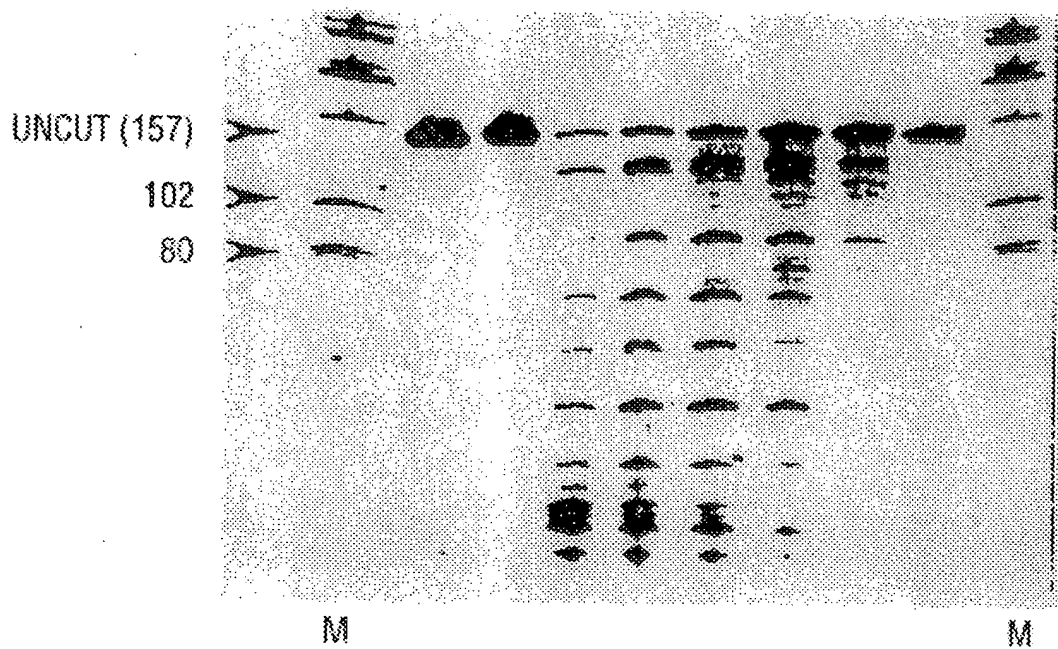
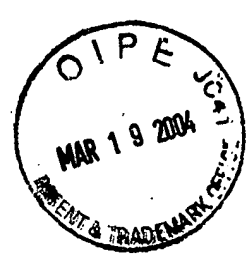


FIG. 37



CLEAVASE™BN (ng): — 10 50 100 250

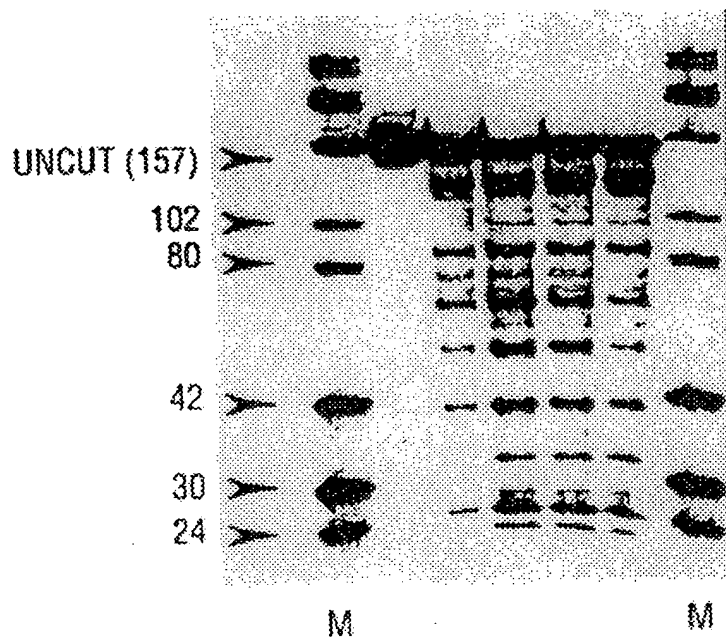


FIG. 38

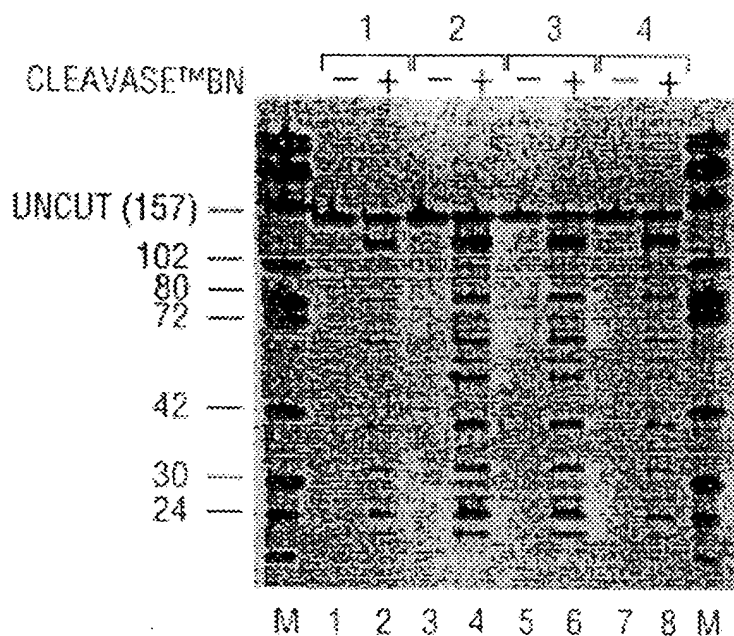


FIG. 39



STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

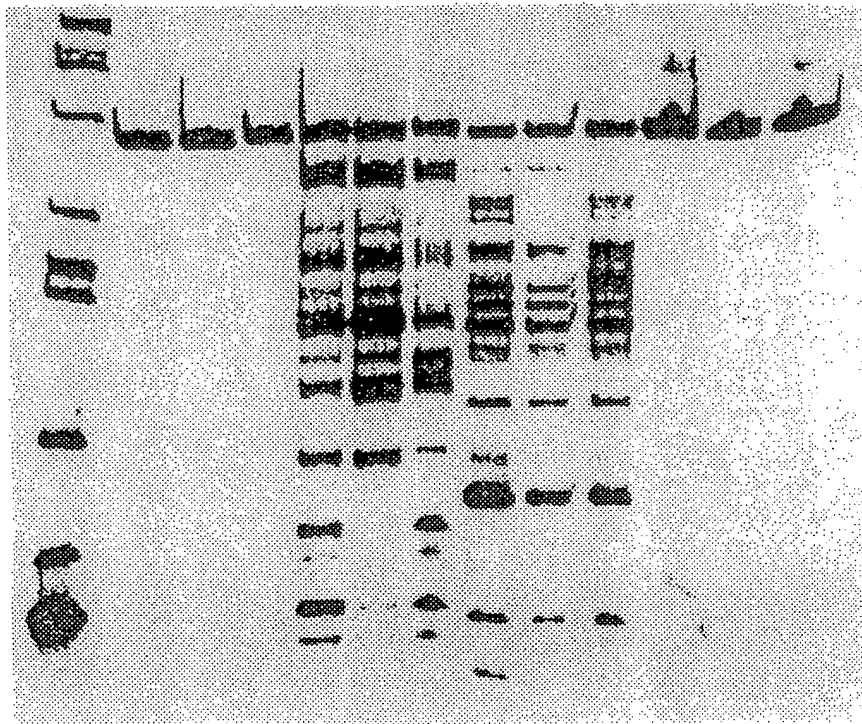


FIG. 40



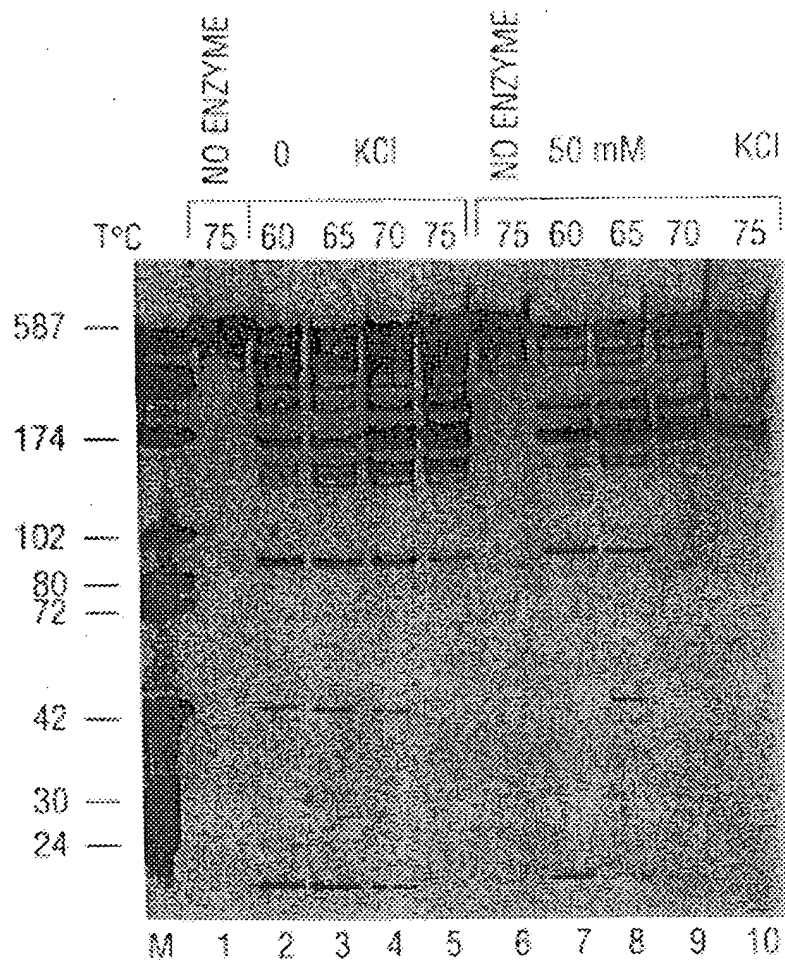


FIG. 41

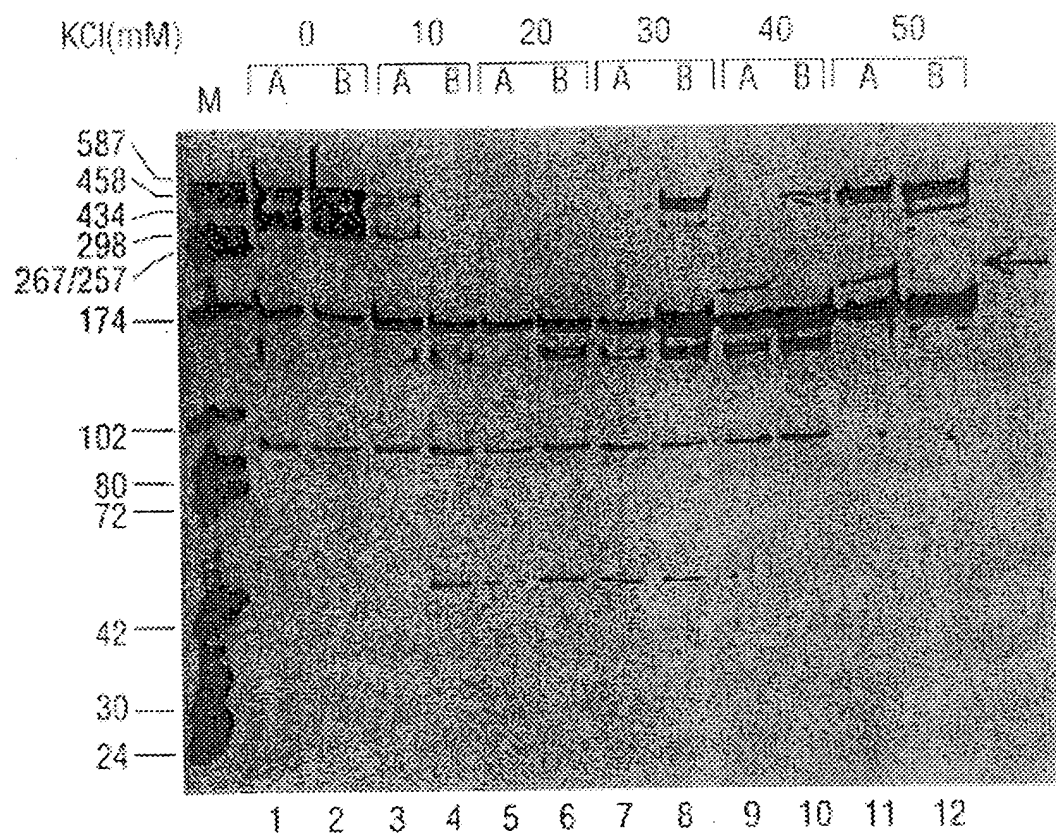


FIG. 42

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CLEAVASE™BN

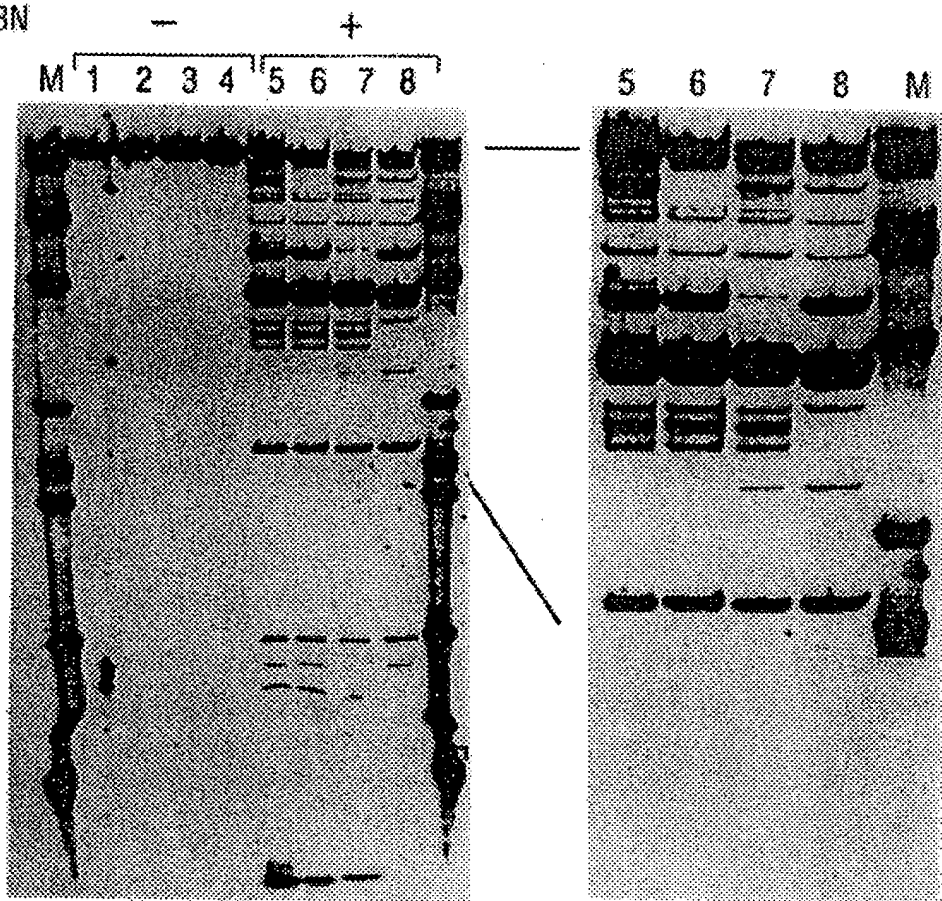


FIG. 43

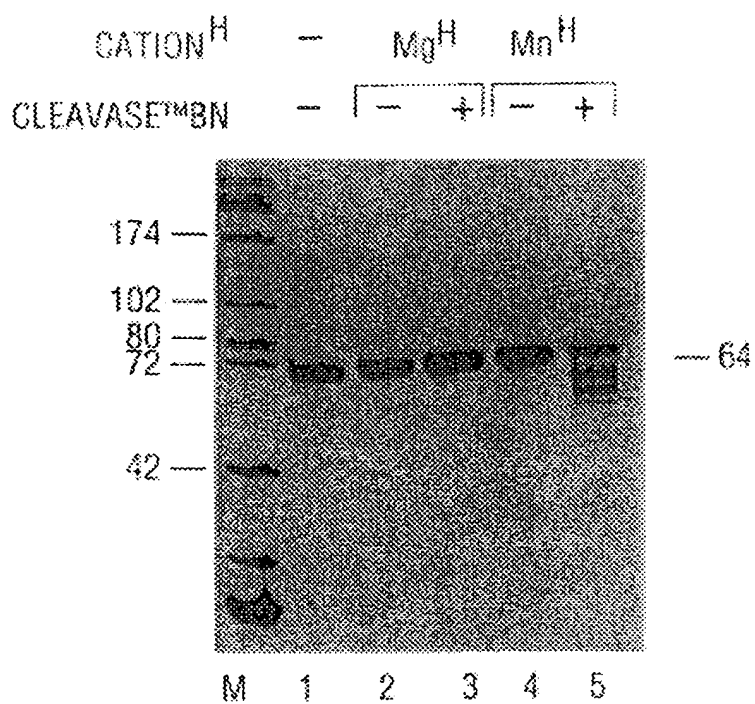


FIG. 44

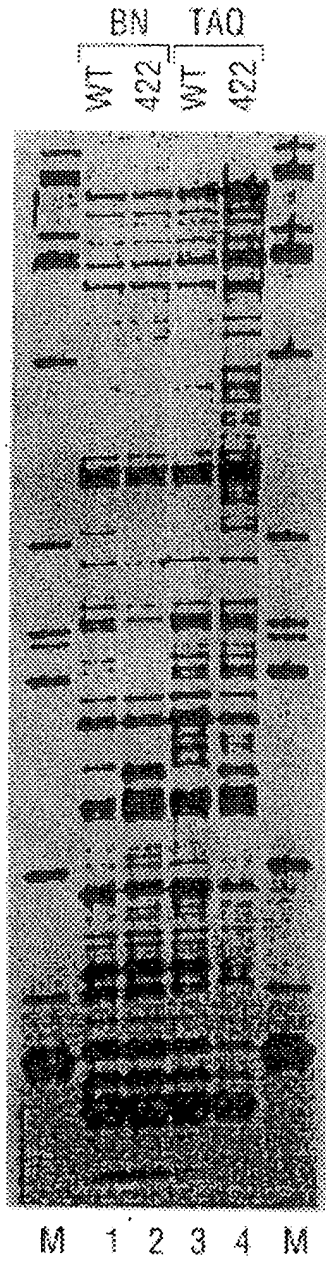


FIG. 45

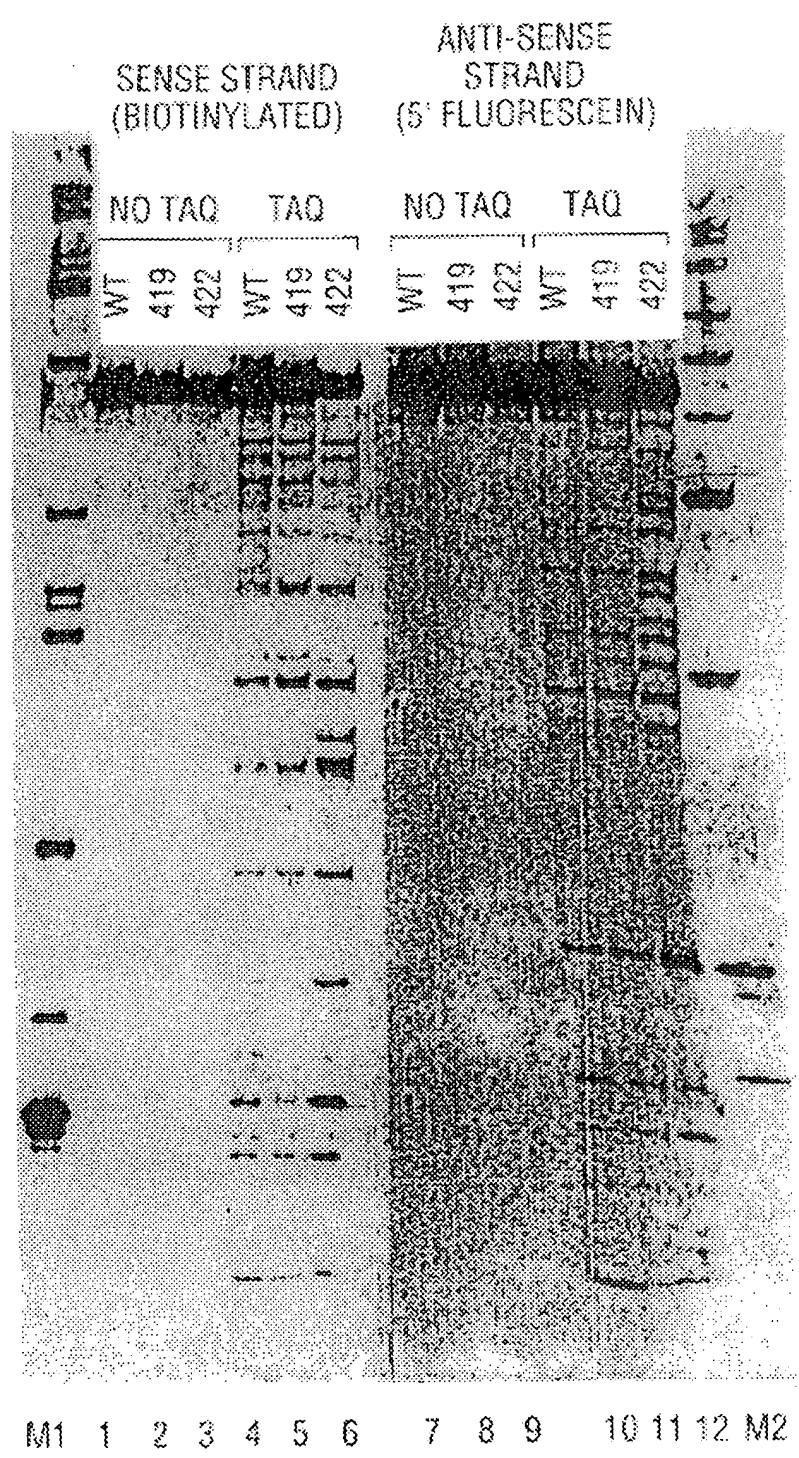


FIG. 46

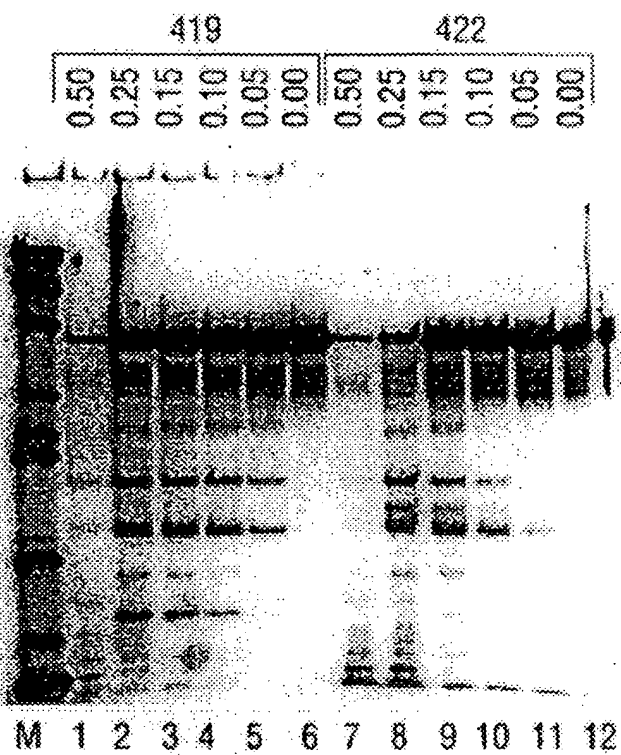


FIG. 47

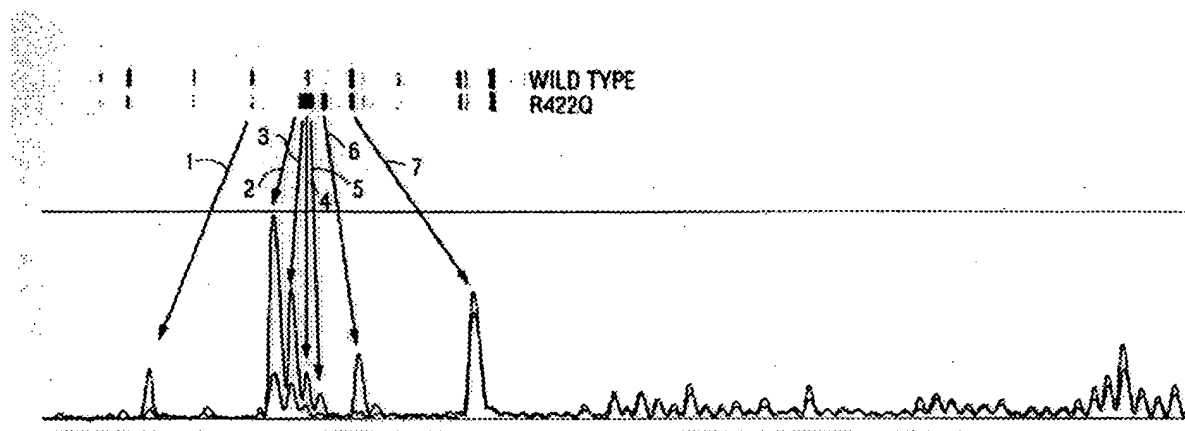


FIG. 48





50

L.100.8-1            5'GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 76) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

L.46.16-10           5'GGCTGACAAGGAAGAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 77) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12           5'GGCTGACAAGGAAGAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 78) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3            5'GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 79) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

L.CEM/251           5'GGCTGACAAGGAAGAACTCGCTGAACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 80) 3'CCGACTGTTCTTCCTTTGAGCGACTTTGTCTCCCTGAAAGGTGTTCCCC

L.36.8-3            5'GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
(SEQ ID NO: 81) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

FIG. 49A



100

L.100.8-1 (SEQ ID NO: 76)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA
L.46.16-10 (SEQ ID NO: 77)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L.46.16-12 (SEQ ID NO: 78)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L19.16-3 (SEQ ID NO: 19)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA
L.CEM/251 (SEQ ID NO: 80)	ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT TACAATGCCCCCTCCATGACCCCTTCTCGGCCAGCCCTTGCGGGTGAAAGA
L.36.8-3 (SEQ ID NO: 81)	ATGTTACGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA

FIG. 49B

150

L. 100.8-1	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGGA 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L. 46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGGA 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L. 46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGGA 3'ACCCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L. 19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGGA 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L. CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGGA 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L. 36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCGGGA 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

**FIG. 49C**



L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	200
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D





250

L. 100. 8 -1 (SEQ ID NO: 76) 5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGG  
3'TCGGACCCACAAAGGACCATCTGAGAGTGGTCGTGAACCGGCCACGACCC

L. 46. 16-10 (SEQ ID NO: 77) 5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTAGCCAGTGCTGGG  
3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAATCGGTCACGACCC

L. 46. 16-12 (SEQ ID NO: 78) 5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCAGTGCTGGG  
3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGTCACGACCC

L. 19. 16-3 (SEQ ID NO: 79) 5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGG  
3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

L. CEM/251 (SEQ ID NO: 80) 5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGG  
3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

L. 36. 8-3 (SEQ ID NO: 81) 5'AGCCTGAGTGTTCCCTGCTAAACTCTCACCAGCACTTGGCCGGTGCTGGG  
3'TCGGACTCACAAGGACGATTTGAGAGTGGTCGTGAACCGGCCACGACCC

HAIRPIN

FIG. 49E





350

L.100.8-1 5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'  
3'TAAATCTTCATCCGGTCACACACACAAGGGTAGAGGATCGGCGGGGAC C 5'

L.46.16-10 5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'  
3'TAAATCTTCATTCCGGTCACACACACAAGGGTAGAGGATCGGCGGGGAC C 5'

L.46.16-12 5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'  
3'TAAATCTTCATTCCGGTCACACACACAAGGGTAGAGGATCGGCGGGGAC C 5'

L.19.16-3 5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'  
3'TAAATCTTCATCCGATCACACACACAAGGGTAGAGGATCGGCGGGGAC C 5'

L.CEM/251 5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'  
3'TAAATCTTCATTCCGATCACACACACAAGGGTAGAGGATCGGCGGGGAC C 5'

L.36.8-3 5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'  
3'TAAATCTTCATCCGATCACACACACAAGGGTAGAGGATCGGCGGGGAC C 5'

FIG. 49G

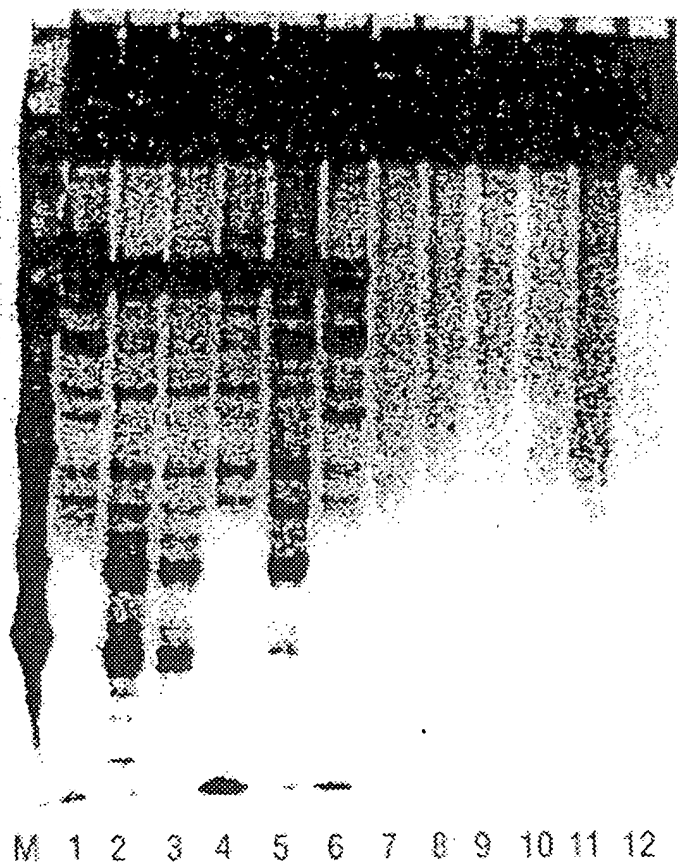


FIG. 50



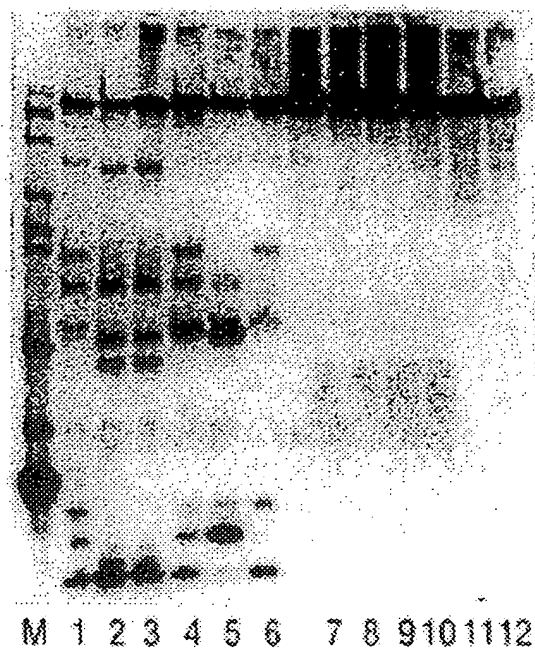


FIG. 51

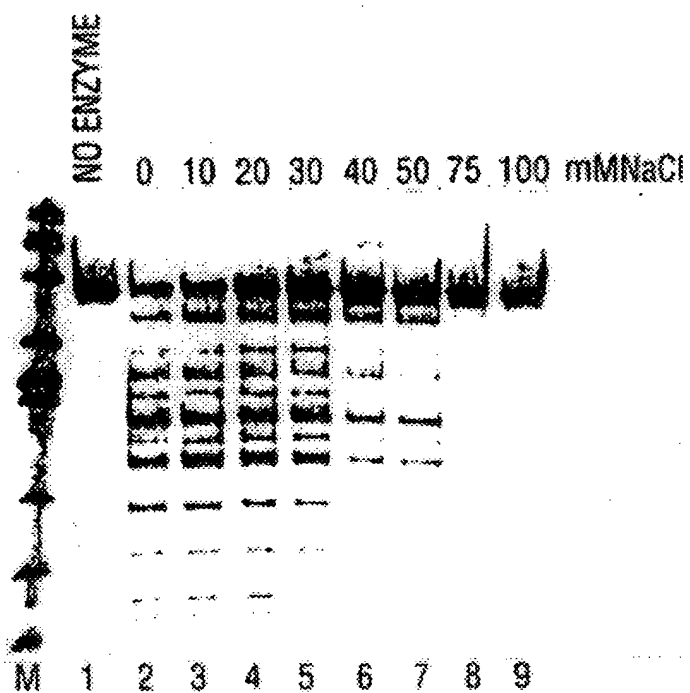


FIG. 52

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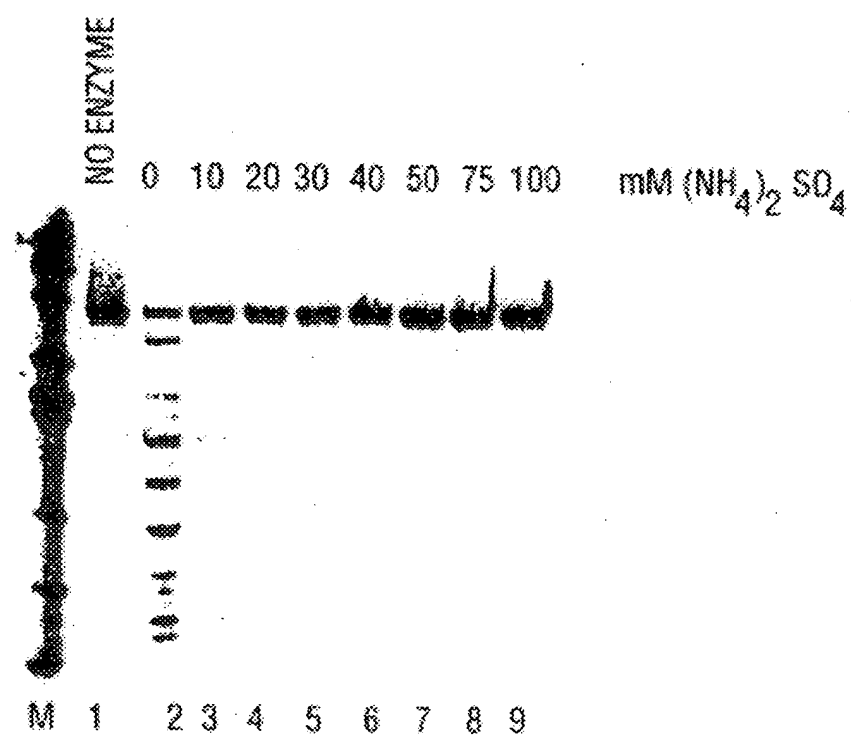


FIG. 53

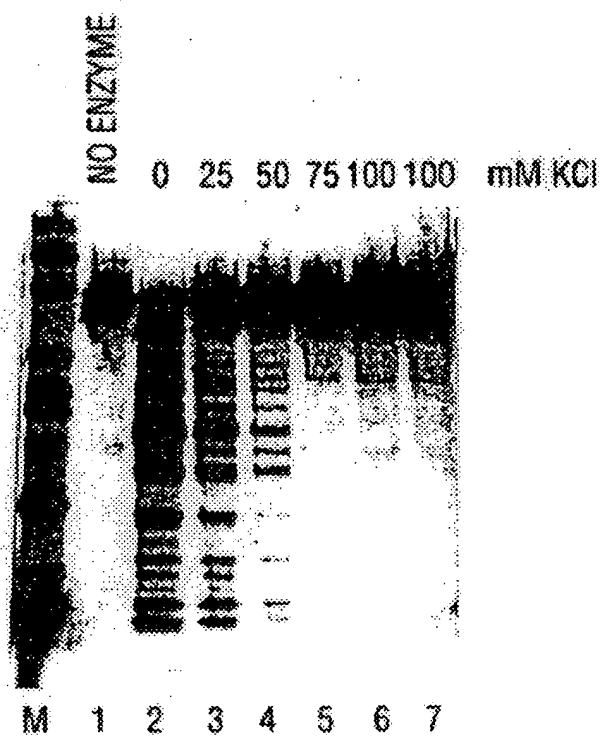


FIG. 54

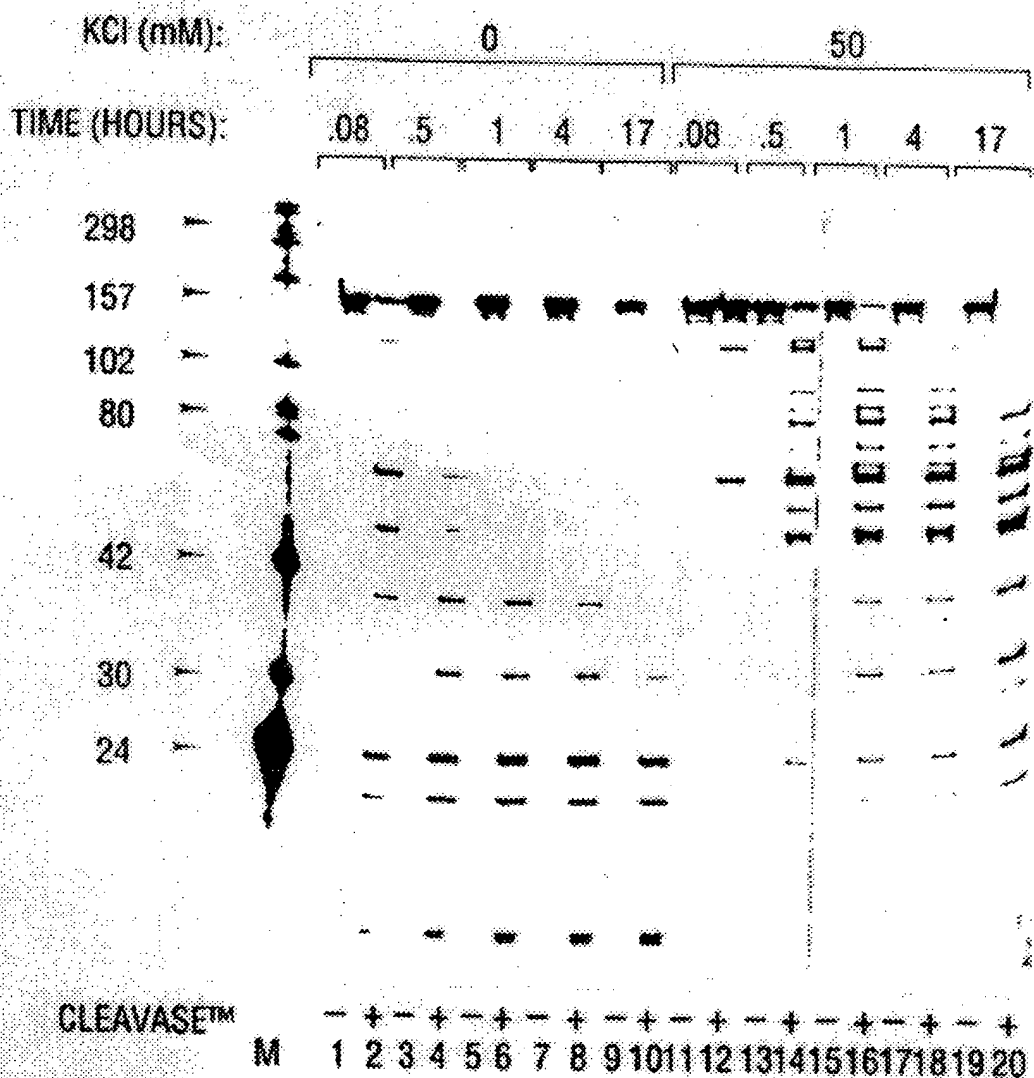


FIG. 55

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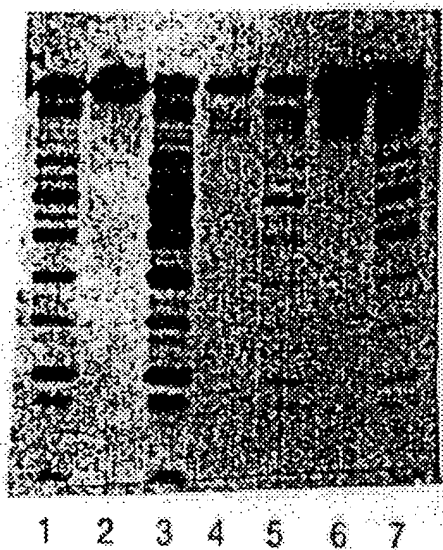


FIG. 56

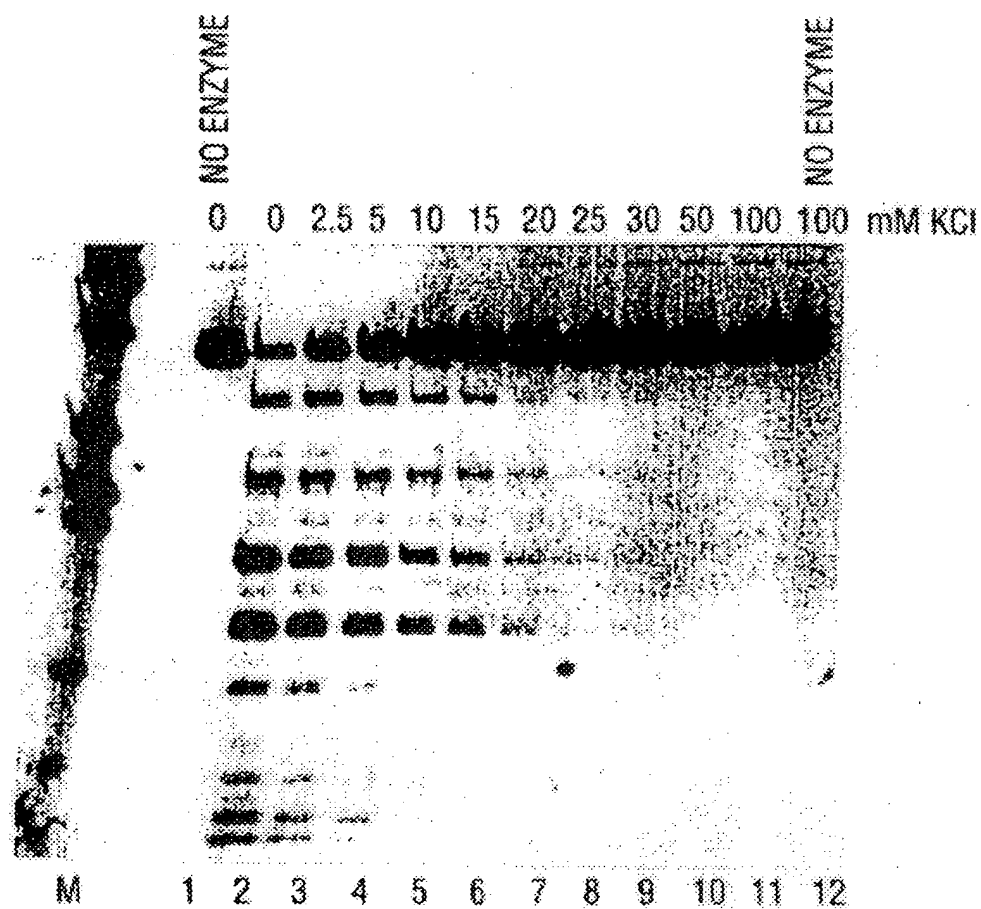


FIG. 57

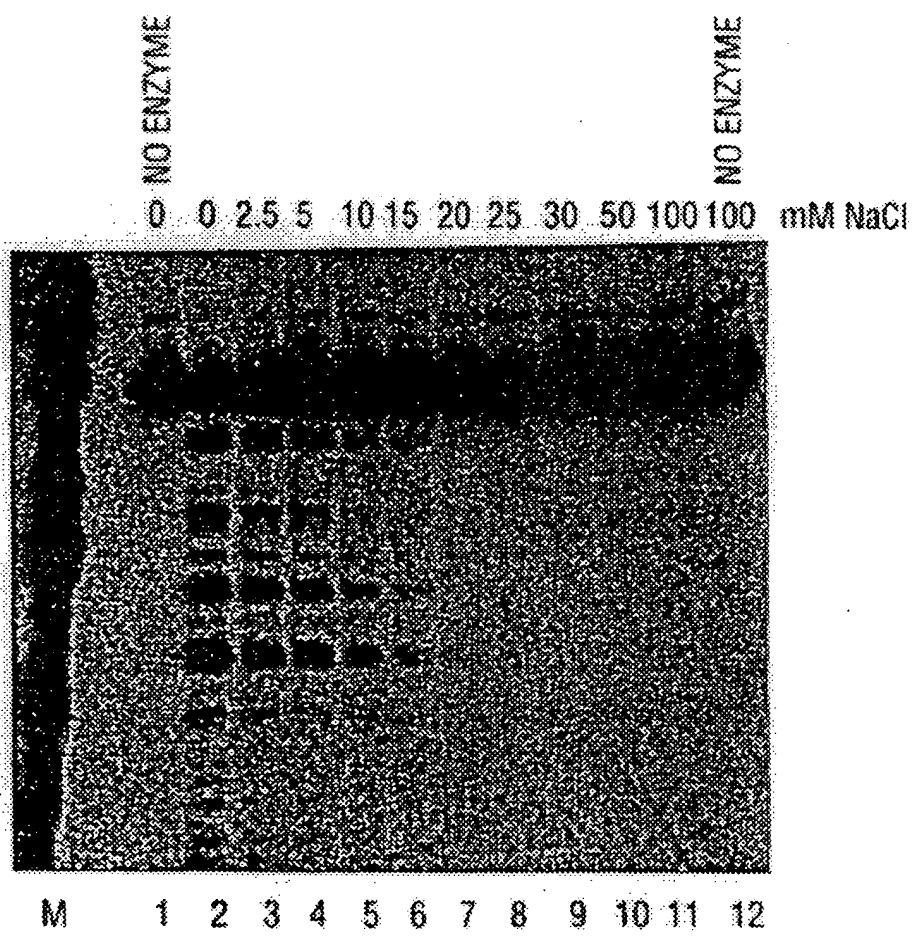


FIG. 58



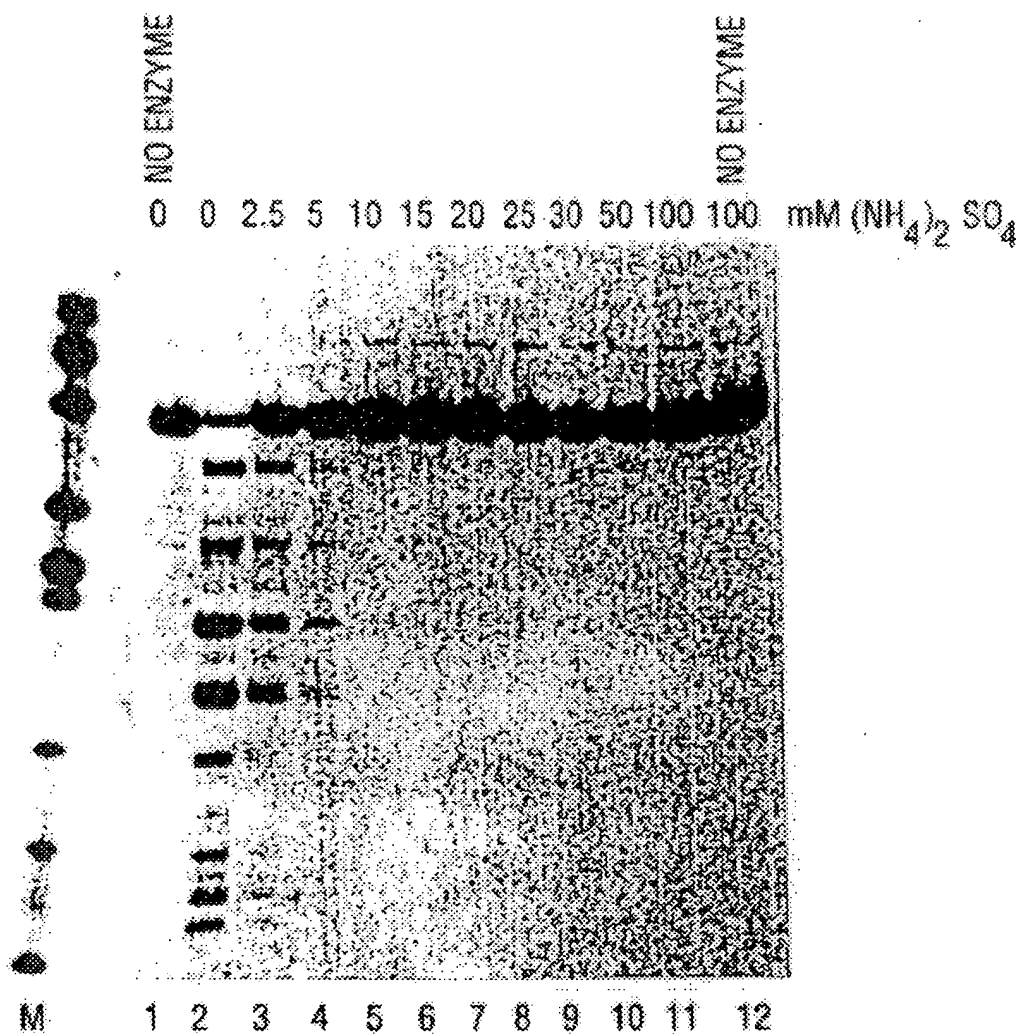


FIG. 59

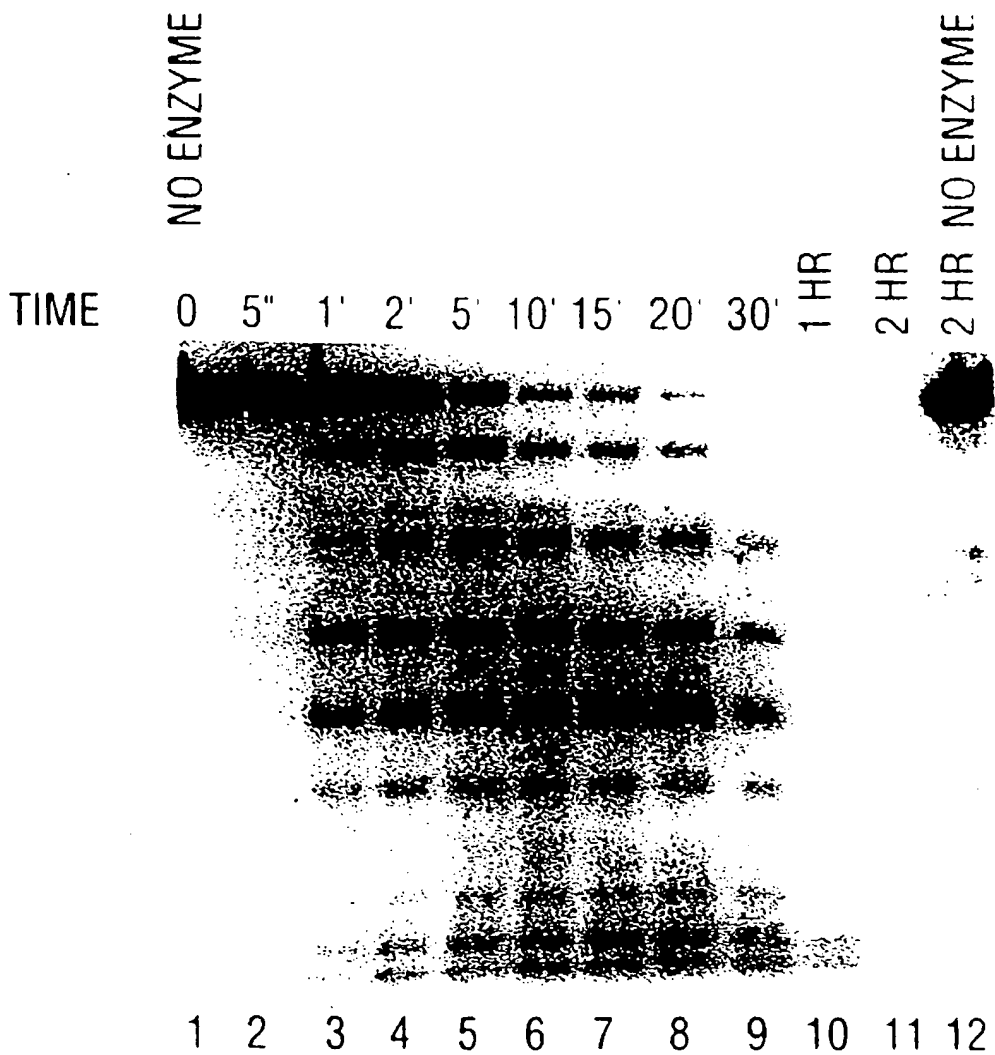


FIG. 60

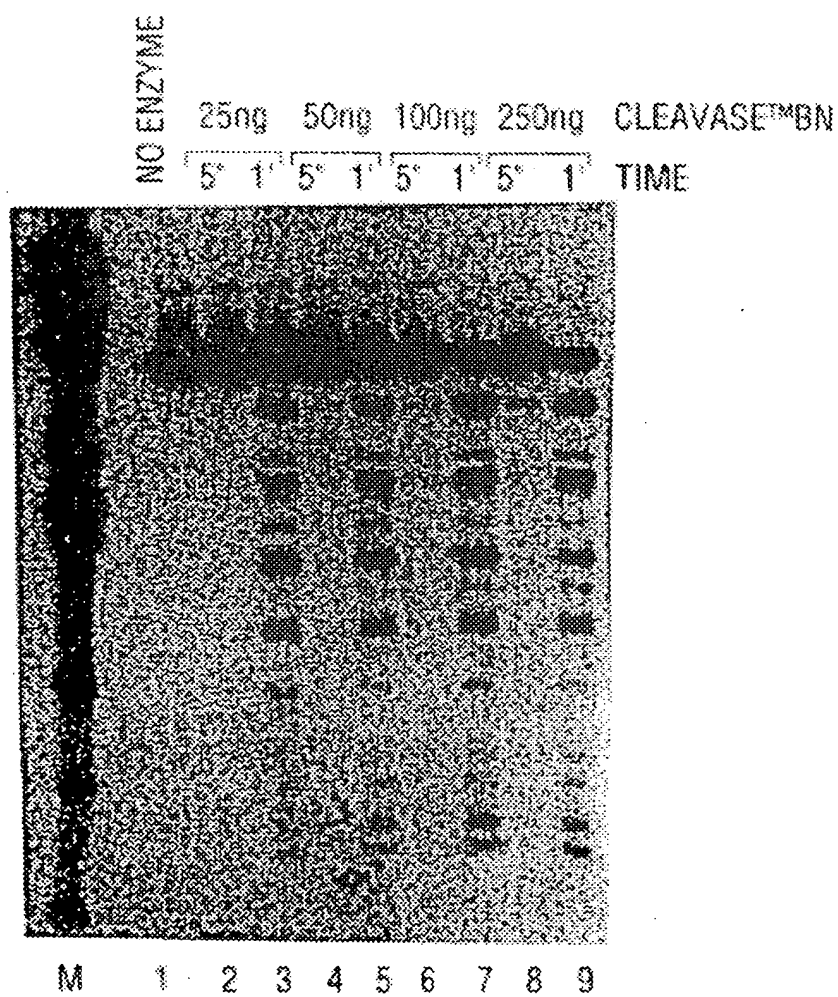


FIG. 61

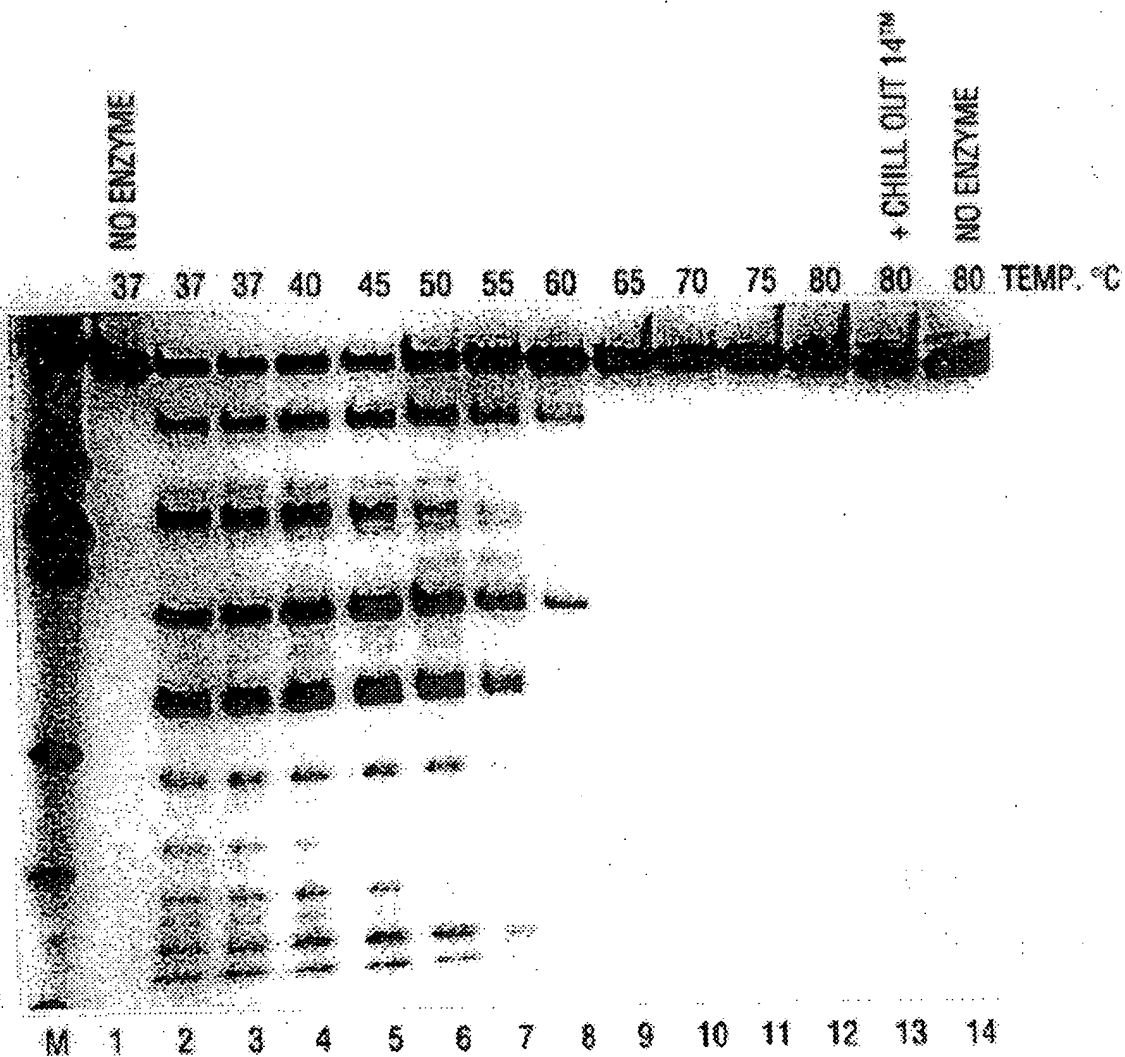


FIG. 62

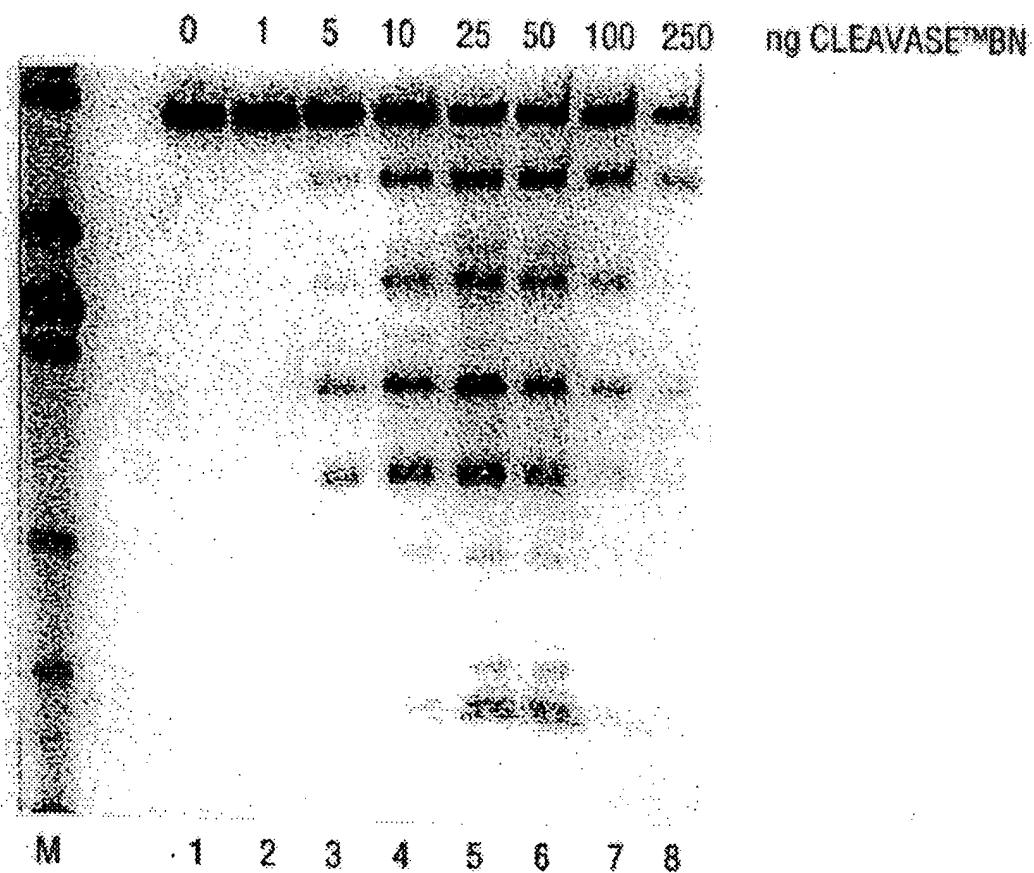


FIG. 63

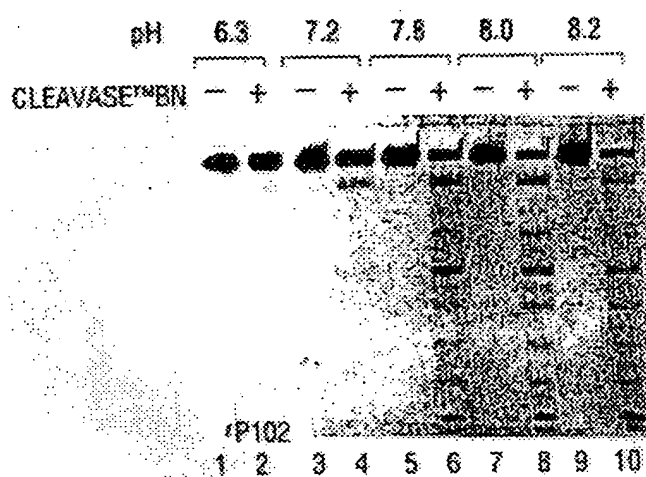


FIG. 64A

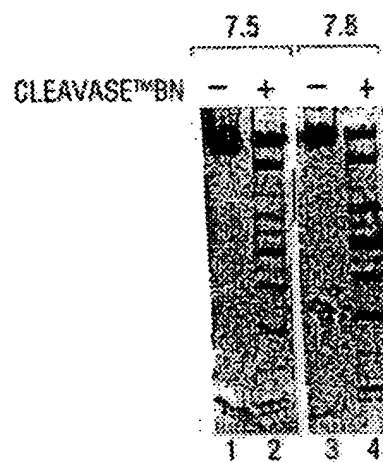


FIG. 64B

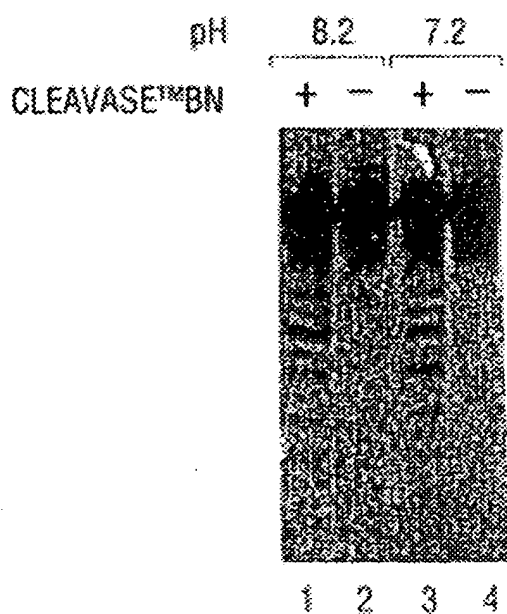


FIG. 65A

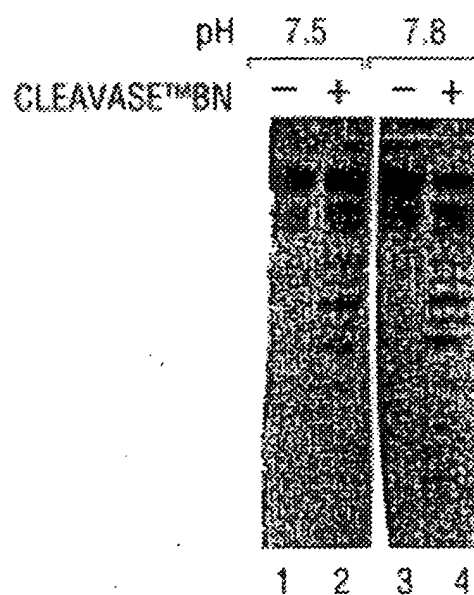


FIG. 65B

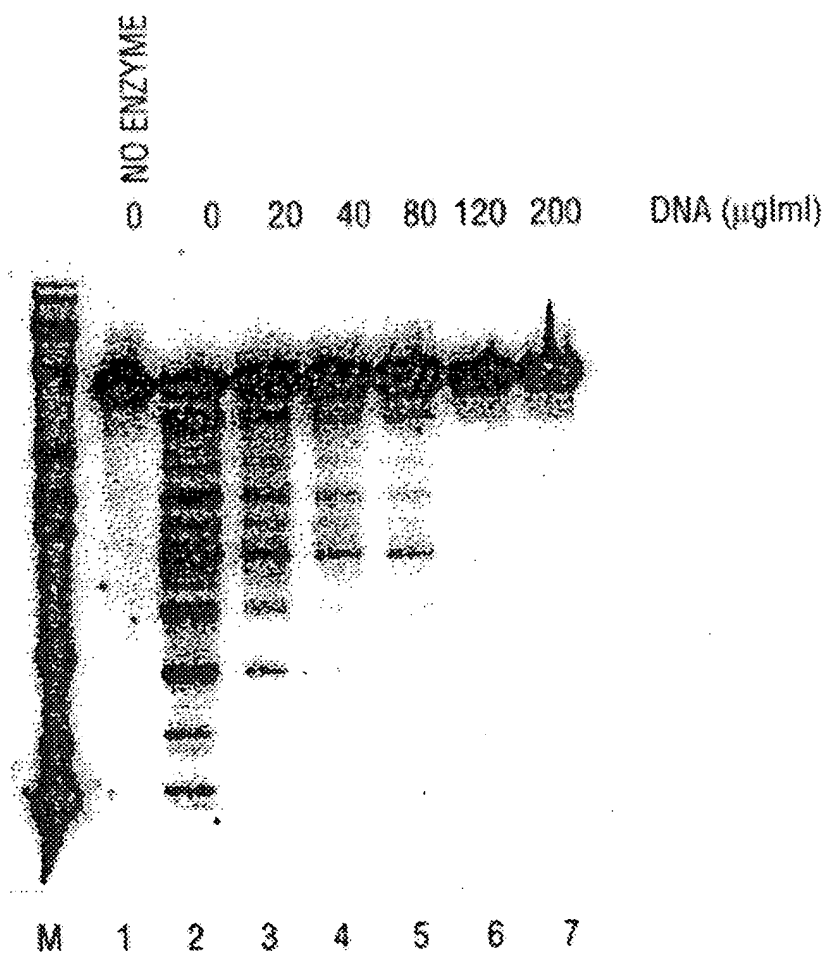


FIG. 66



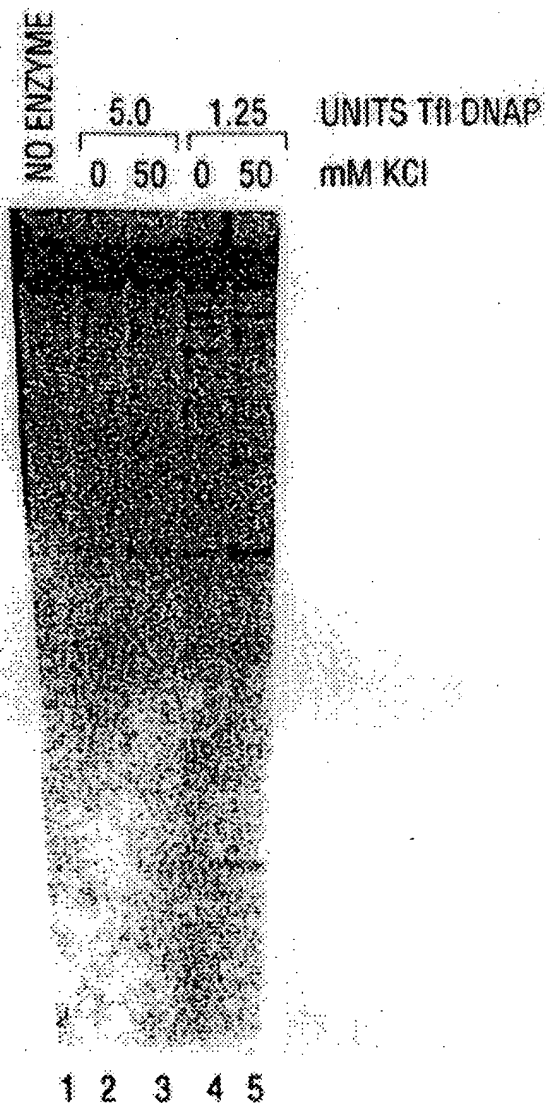


FIG. 67

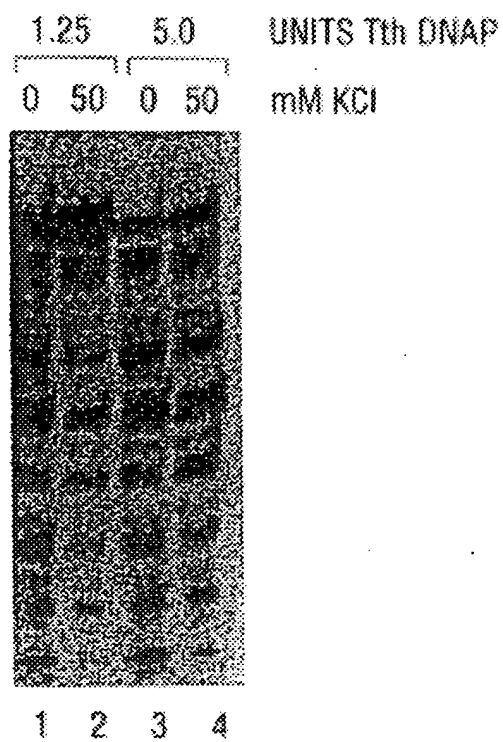


FIG. 68

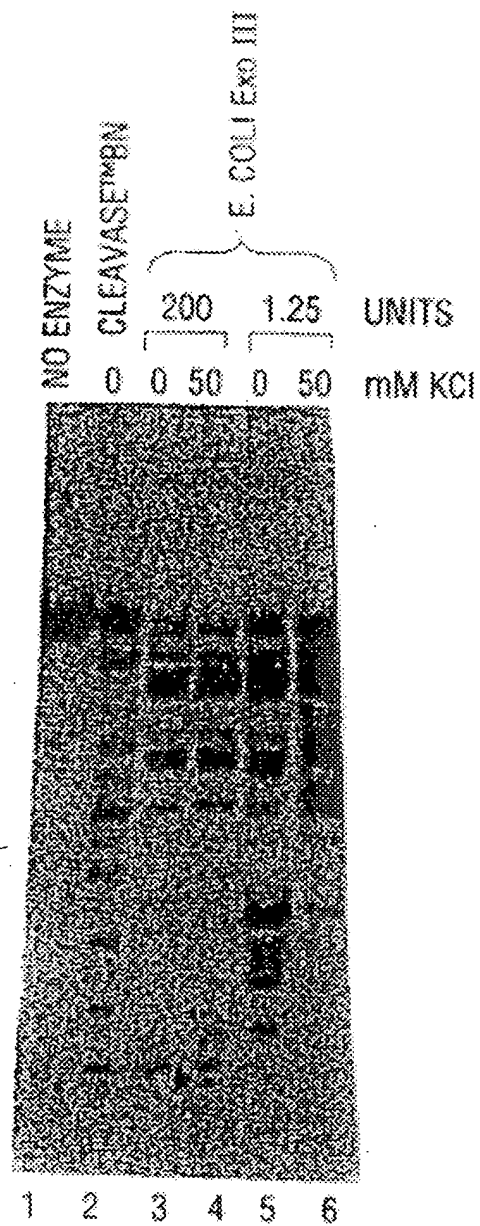


FIG. 69

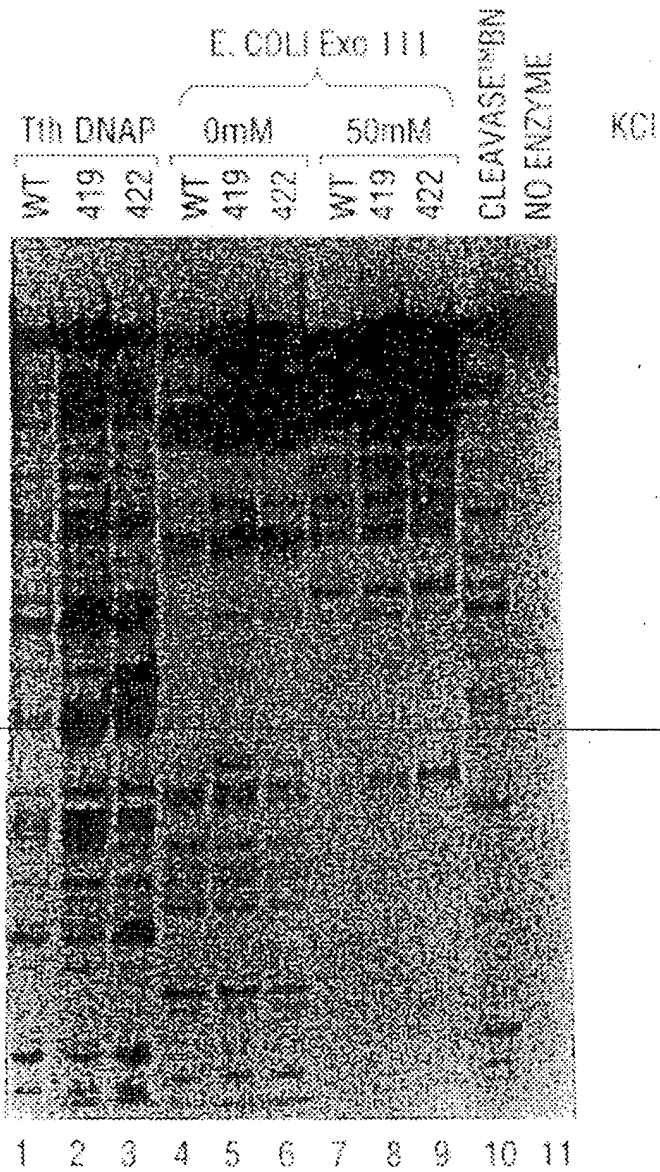
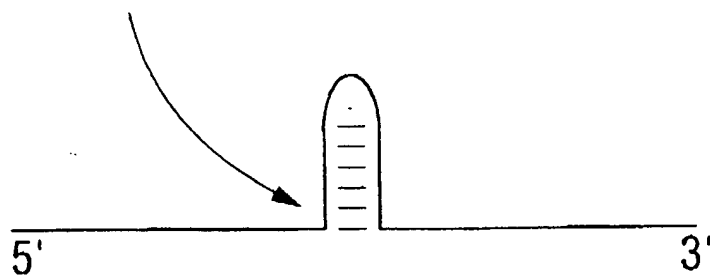


FIG. 70



5' CLEAVAGE SITE



3' CLEAVAGE SITE

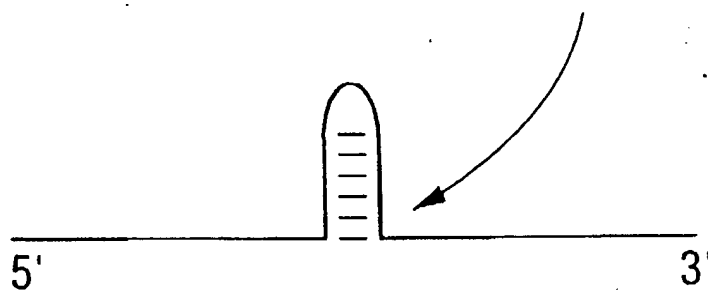


FIG. 71

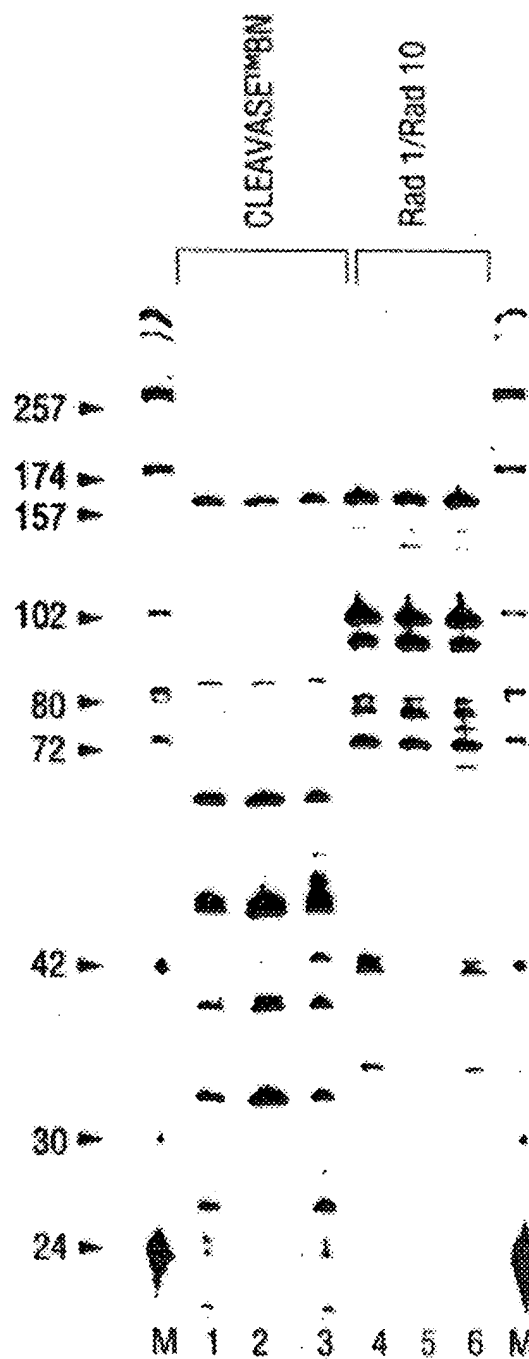


FIG. 72



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FIG. 73

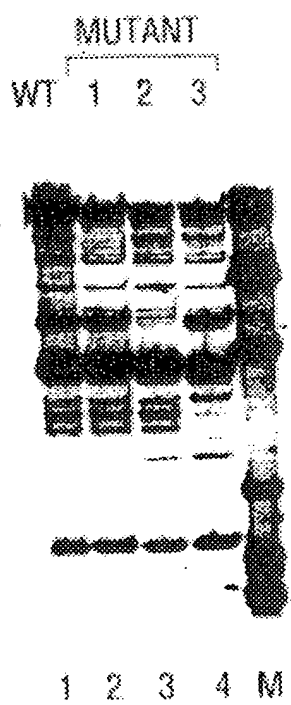


FIG. 74A

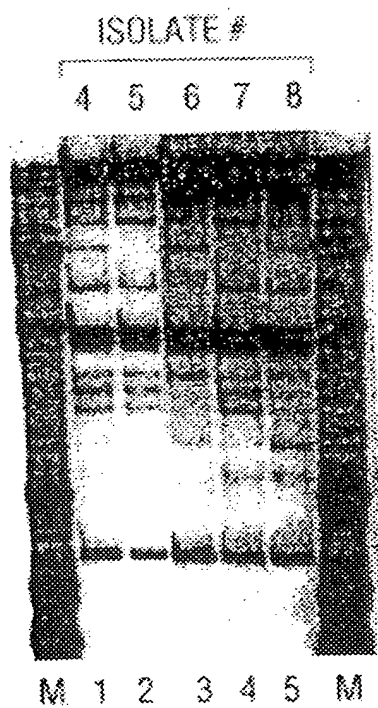


FIG. 74B



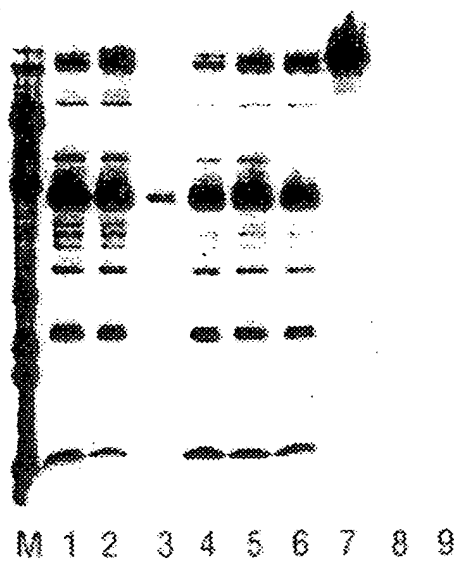


FIG. 75



% OF TOTAL  
MUTATIONS

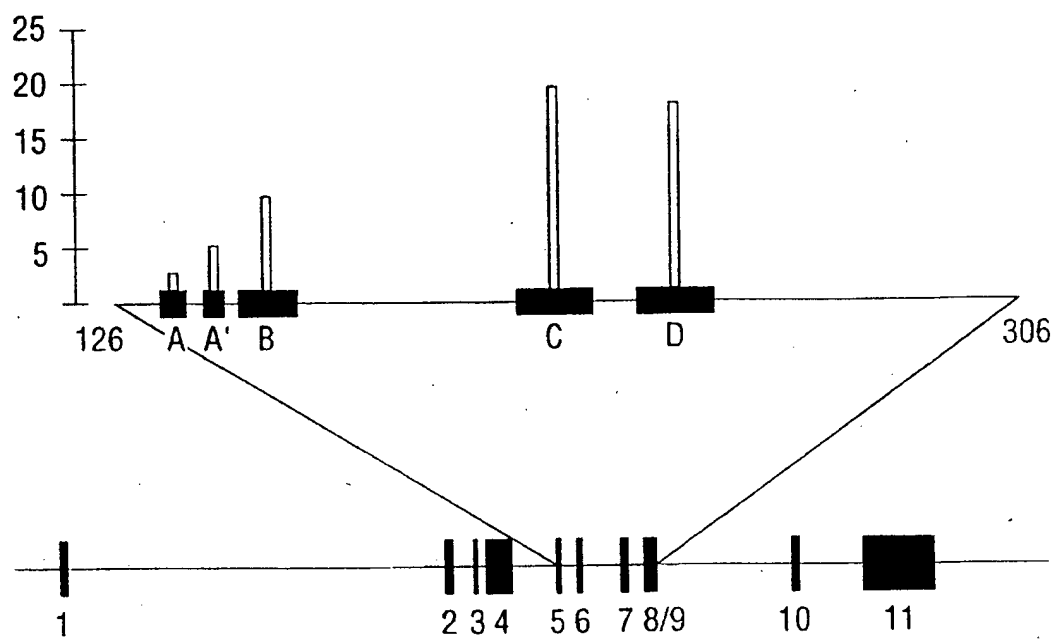


FIG. 76

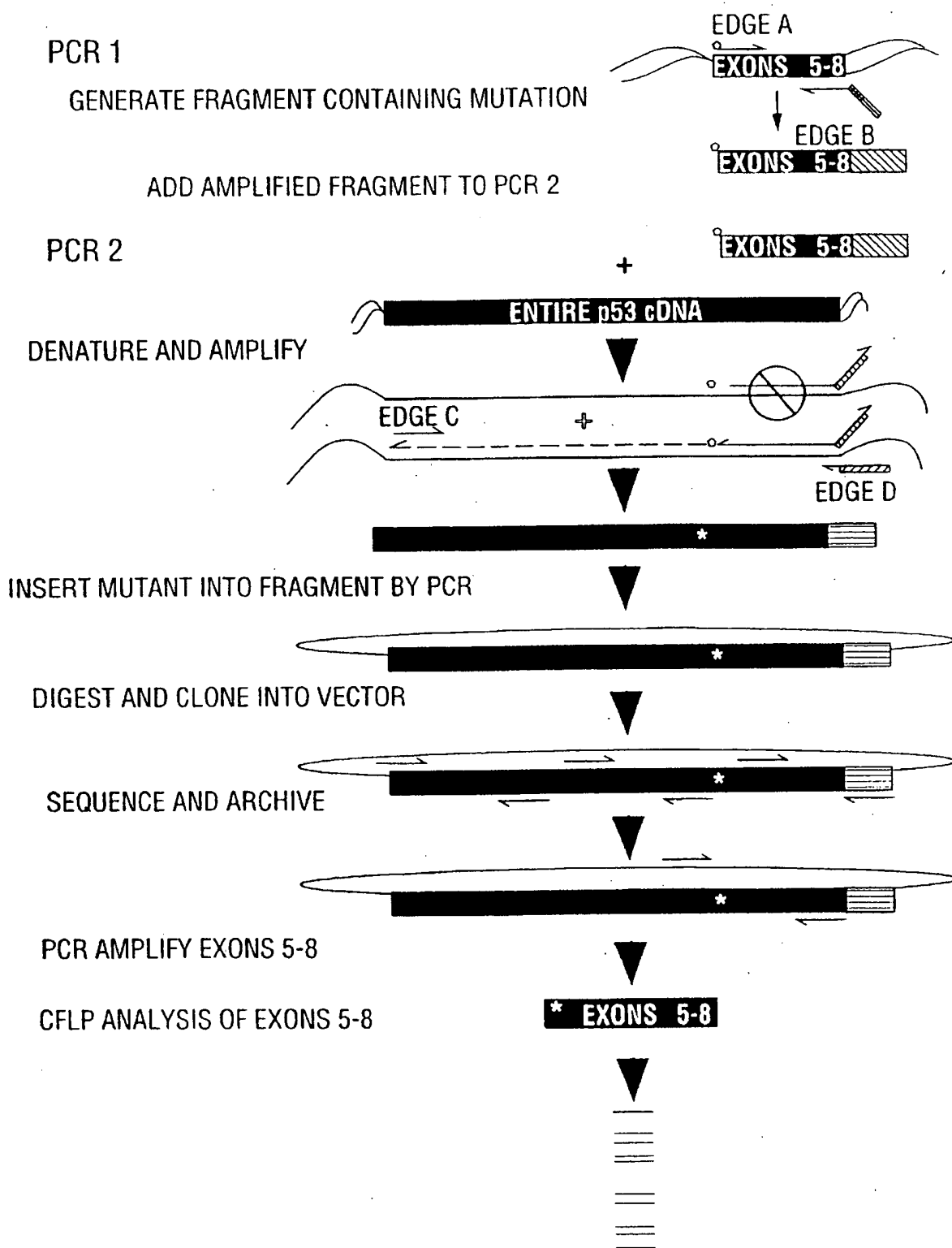


FIG. 77

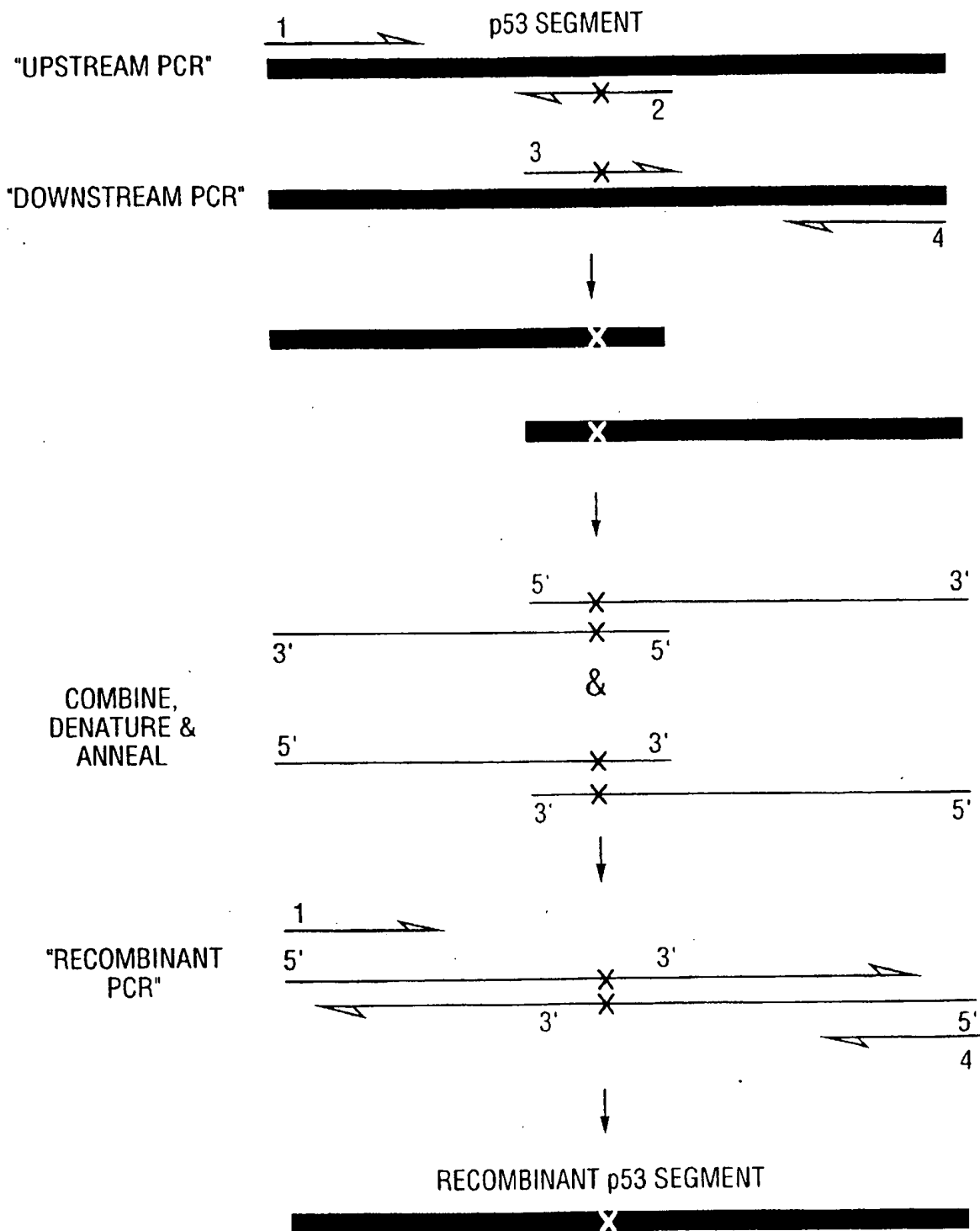


FIG. 78

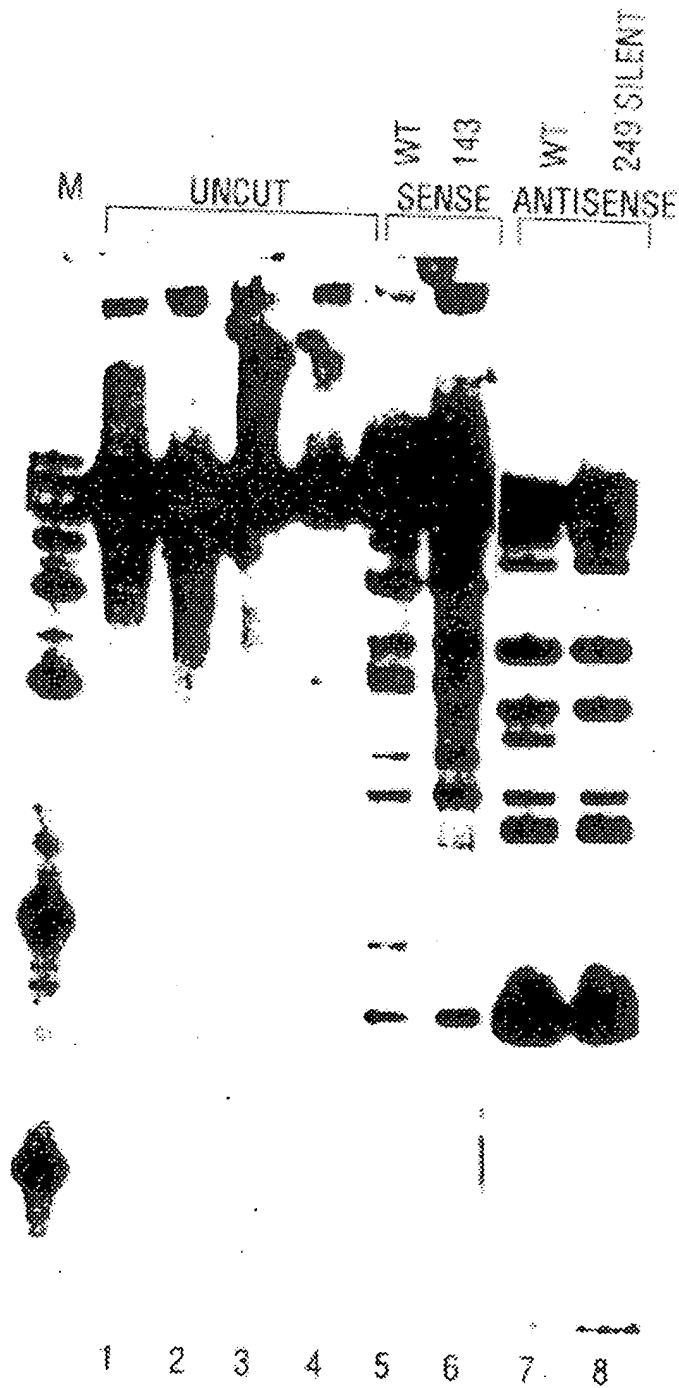


FIG. 79

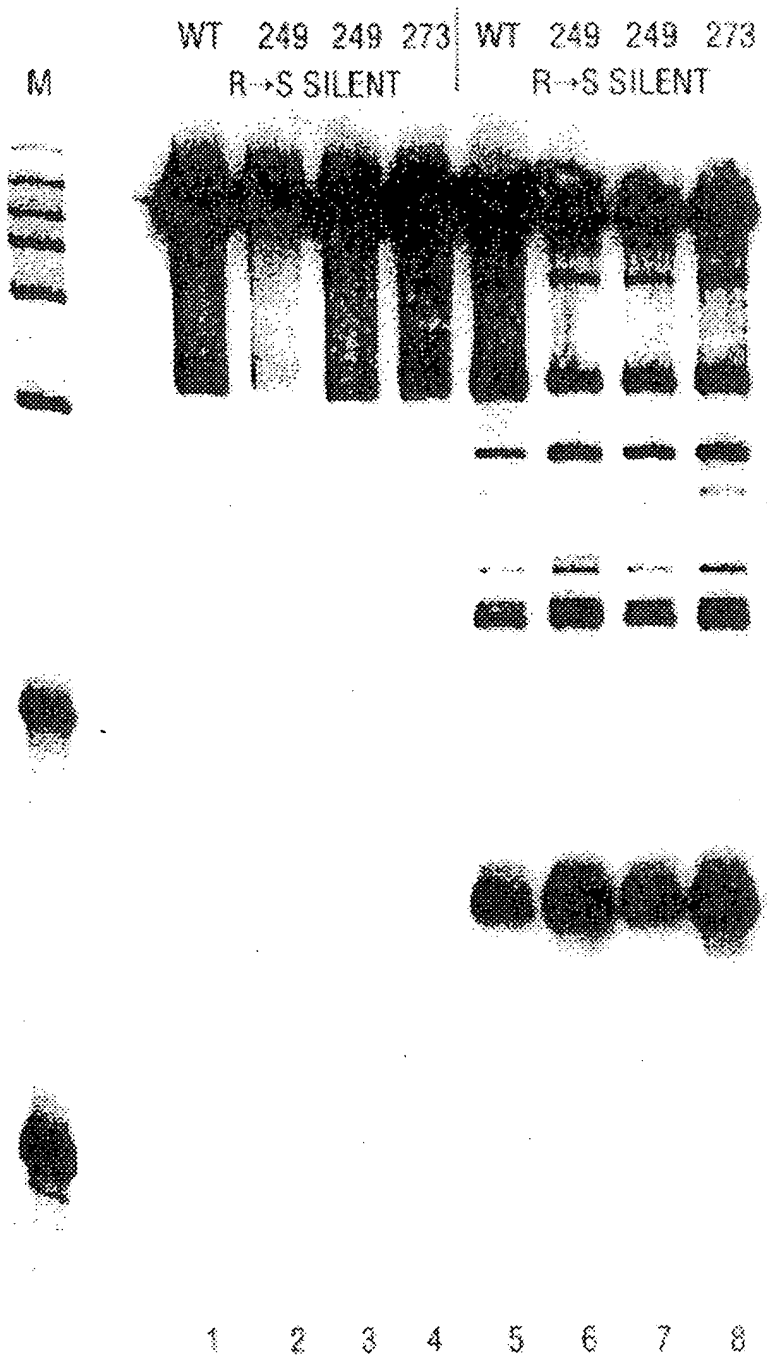


FIG. 80

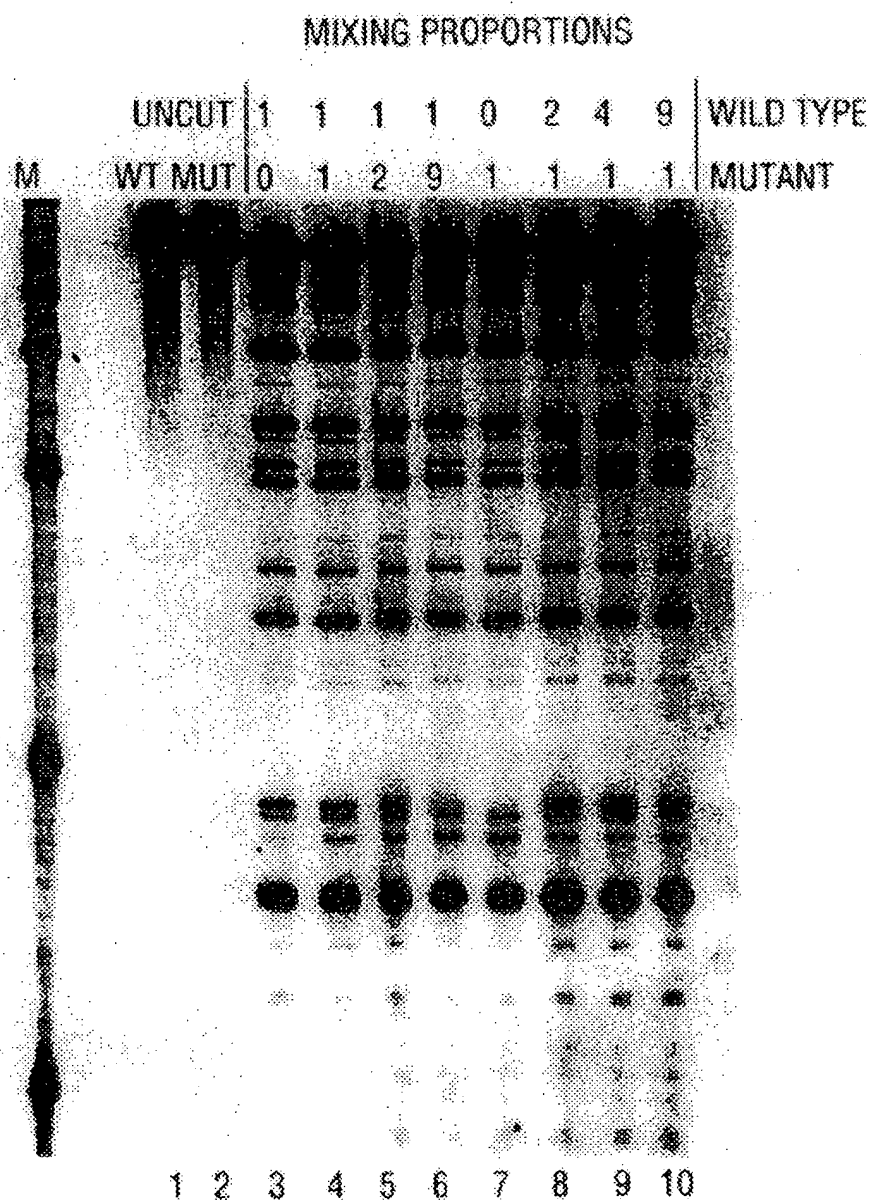


FIG. 81



HCV1.1	(SEQ ID NO:121)	1	CTGTCTTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTTCAC	GCAGAAAGCG	CCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCCGGAGAG	CCATAGTGGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	GTGGATGIAA	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	
HCV7.1			GGTGAGTACA	CCGGAATTGC	IGGGGIGACC	GGGTCCTTTC	TTGGAG-CAA	

FIG. 82A





HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	GCGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	GCGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	GCGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	GCGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	GCGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	GCGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

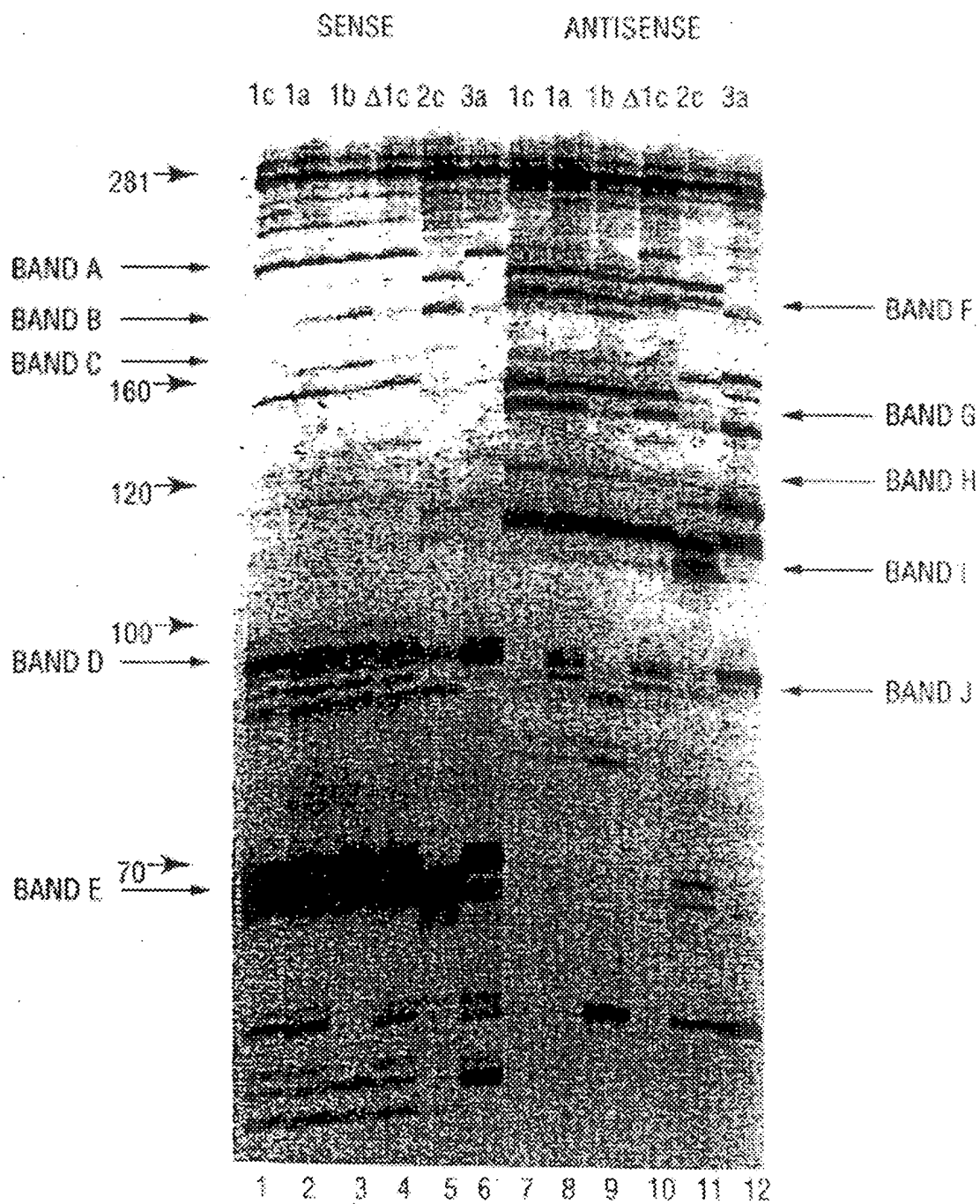


FIG. 83

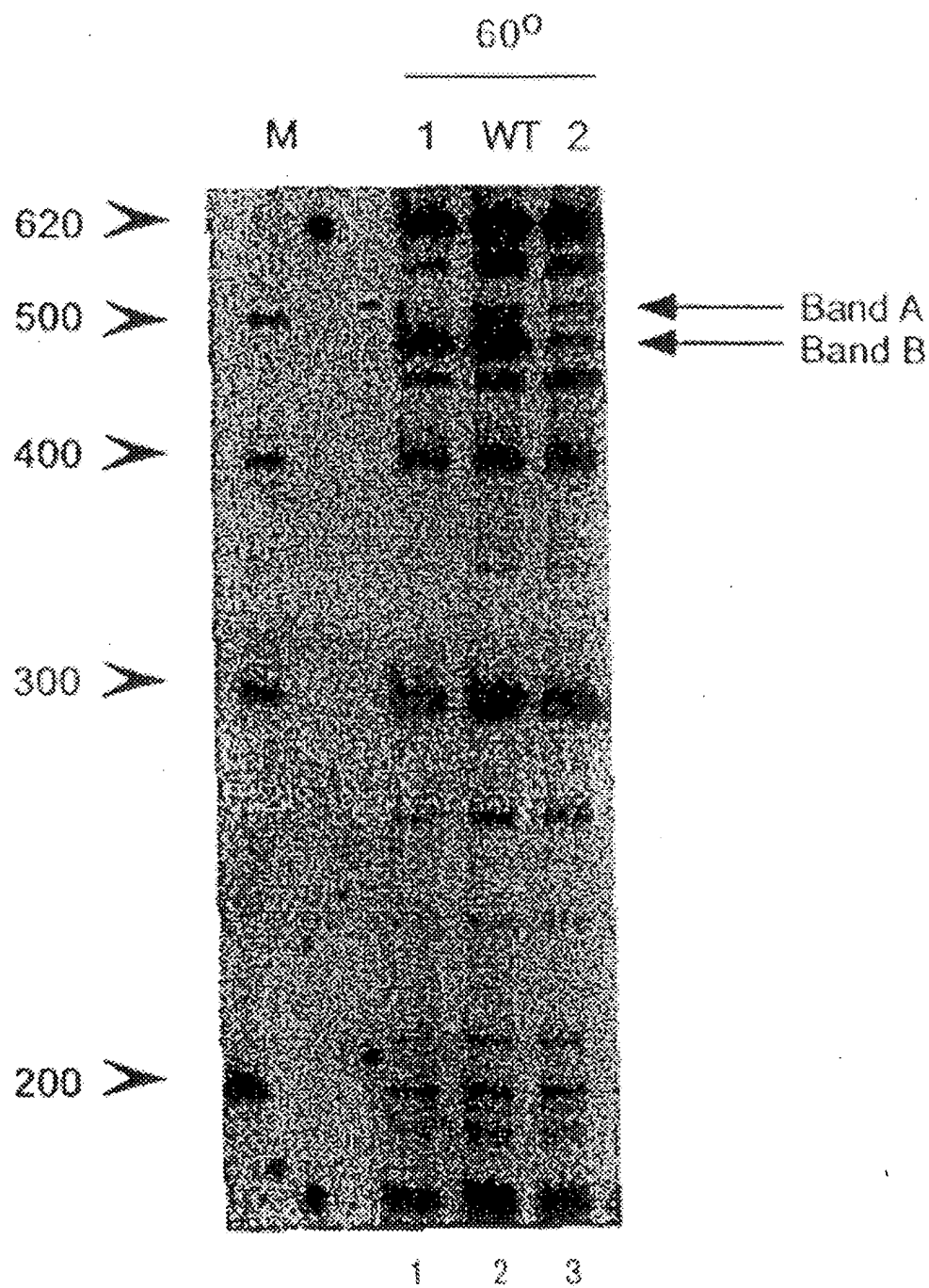


FIG. 84

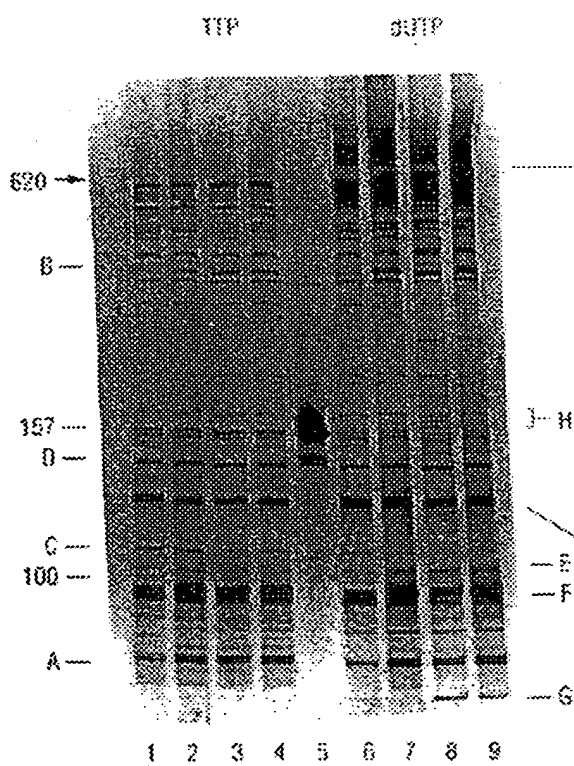


FIG. 85A

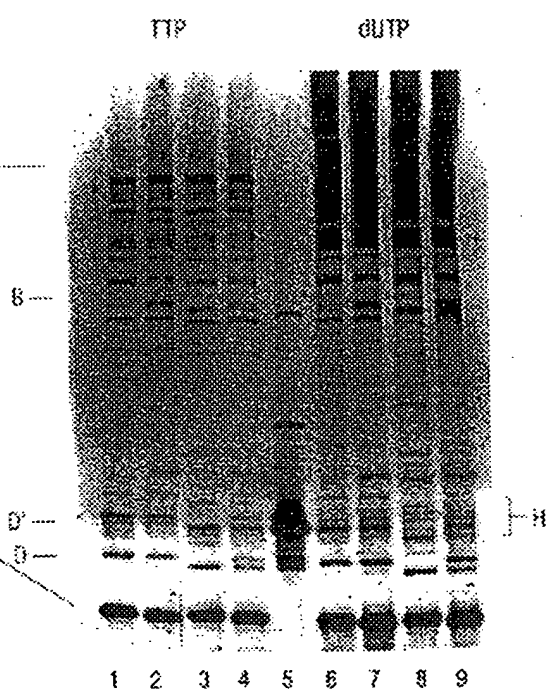


FIG. 85B

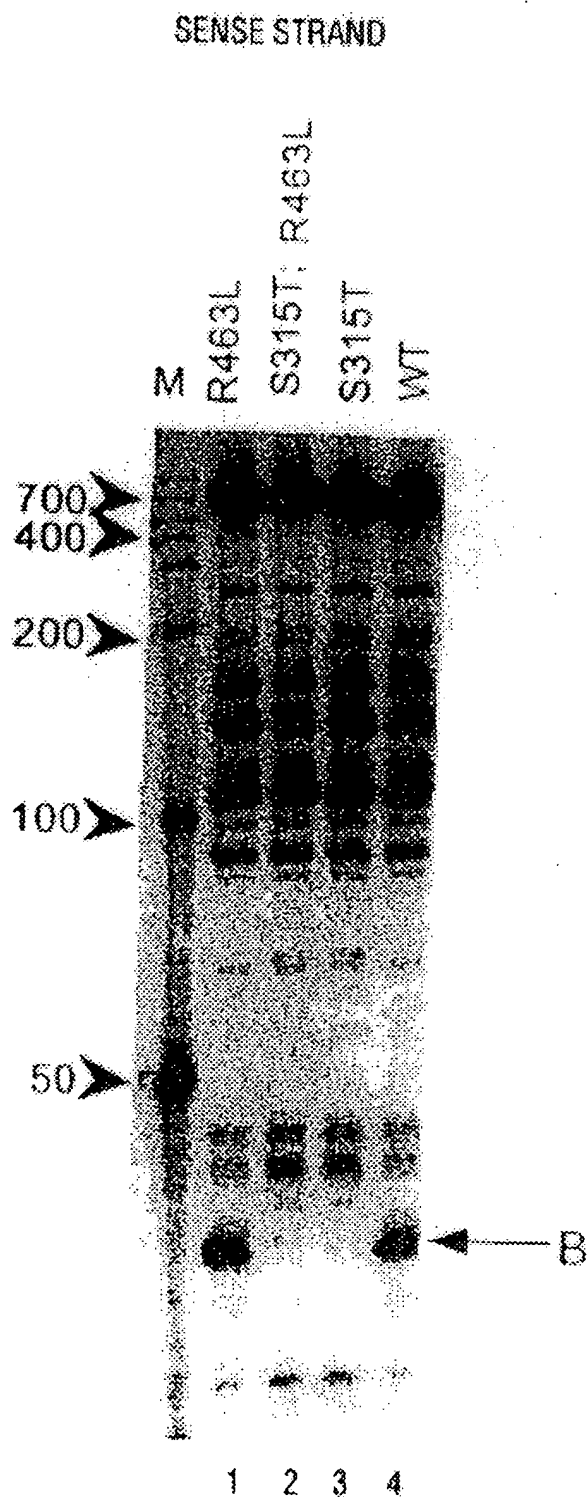


FIG. 86

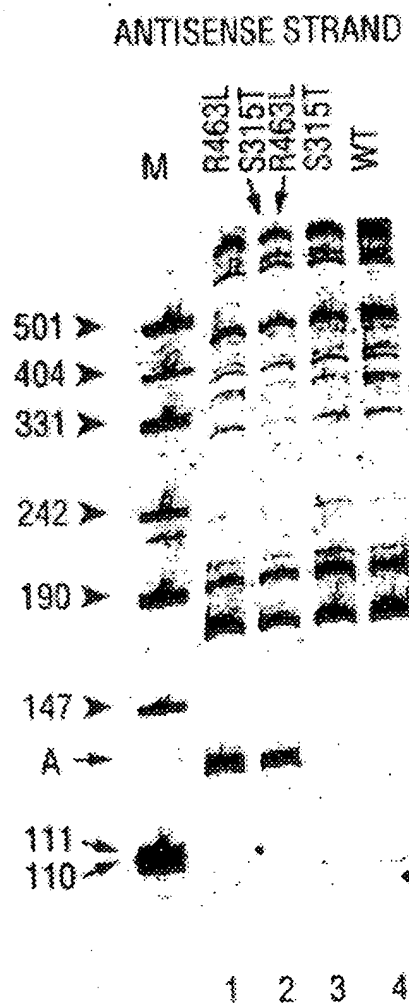


FIG. 87



10 20 30 40 50 60  
AGA GTTTGATCCT GGCTCAG  
AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA  
TTTAACTTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CCGTCCGGAT TGTGTACGTT

70 80 90 100 110 120  
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA  
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG AACGACTGC TCACCGCCTG CCCACTCAT

130 140 150 160 170 180  
TGCTCTGGAA ACTGCCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT  
ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA

190 200 210 220 230 240  
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCCAGATG  
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG CCCGGAGAAC GTAGCCTAC ACGGGTCTAC

250 260 270 280 290 300  
GGATTAGCTA GTAGGTGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA  
CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT

310 320 330 340 350 360  
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG  
CCTACTGGTC GGTGTGACCT TGA CTCTCTGTG CCAGGTCIGA GGATGCCCCC CGTCGTCACC  
TGA GGATGCCCCC CGTCGTC

FIG. 88A



370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCGGACTA	CGTCGGTACG	GGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCGC	ATTTCCGGTG	CGTCCGCCAA	ACAAATTCACT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCACTCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCCGAG	TTGGACCCCT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACCTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCC	CACCCCTCGT

FIG. 88B





790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAAACGAT	GTCGACTTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGG	GCATTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA	CCGAAGGCCT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGACGGGGGC	CCGCACAAGC	GGTGGAGCAT	GTGGTTTAAT
TCCAATTTTG	AGTTACTTA	ACTGCCCCCG	GGCGTGTTG	CCACCTCGTA	CACCAAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTGCCCT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTGAGCT	CGTGTGTGTA
TTACACGGAA	GCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
					SB-1
AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCC	TTTGTGCGCA	GCGGTCCGGC
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCGC
1150	1160	1170	1180	1190	1200
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAACTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGATG	ACGTCAAGTC
GCCCTTGAGT	TTCTCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCAG

FIG. 88C



SB-3  
SB-4

1210	1220	1230	1240	1250	1260
ATCATGGCCC	TTA				
ATCATGGCCC	TTACGA				
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAACGG
<u>TAGTACCGGG</u>	<u>AATGCTGGTC</u>	<u>CCGATGTGTG</u>	<u>CACGATGTTA</u>	<u>CCGCGTATGT</u>	<u>TTCTCTTCGC</u>
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTCCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	<u>CTTACGGTGC</u>	<u>CACIIATGCA</u>
				GC	CACTTATGCA
					1743
1390	1400	1410	1420	1430	1440
TCCCCGGCCT	TGTACACACC	GCCCCGCACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT
<u>AGGGCCCCGA</u>	<u>ACATGTGTGG</u>	<u>CGGGCAGTGT</u>	<u>GGTACCCTCA</u>	<u>CCCAACGTTT</u>	<u>TCITTCATCCA</u>
<u>AGGGCCCCGA</u>	<u>ACATG</u>				
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA
TCGAATTGGA	AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCCA	CTTCAGCATT
1510	1520	1530	1540	1550	
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCTTG	GACGCCAAC	TAGTGGAGGA	AT.....	

FIG. 88D



1638 (SEQ ID NO:151) AGAGTTTGATCCTGGCTCAG  
E.colirrsE (SEQ ID NO:158)0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCA  
Cam.jejun5 (SEQ ID NO:159)0 ~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCCTAATACATGCA  
Stp.aureus (SEQ ID NO:160)0 ..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCCTAATACATGCA

ER10 (SEQ ID NO:152)  
E.colirrsE GGCGGACGGG  
Cam.jejun5  
Stp.aureus  
60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG  
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAGTGGA-----TTAGTGGCGCACGGG  
61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG

ER10  
E.colirrsE TGAGTAA  
Cam.jejun5  
Stp.aureus  
114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGATAACTACTGGAACGGTAGCTAATA  
114 TGAGTAAGGTATAGTTAATCTGCCCCACACAAGAGGACAAACAGTTGGAAACGACTGCTAATA  
113 TGAGTAACACGCTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA

E.colirrsE  
Cam.jejun5  
Stp.aureus  
175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCTCTTG  
176 CTCTATACTCCTGCTTTAACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG  
175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT-----CTT-----GCTGTCA

E.colirrsE  
Cam.jejun5  
Stp.aureus  
221 CCATCGGATGTGCCCCAGATGGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAGGCGACGA  
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA  
229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirrsE  
Cam.jejun5  
Stp.aureus  
283 TCCCTAGCTGGTCTGAGAGGATGACCCAGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA  
283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACGGTCCAGACTCCTA  
291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA  
1659 (COMPL) ACTCCTA

FIG. 89A



E.colirrsE	345	CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
Cam.jejun5	345	CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCTTGACGCAGCAACGCCGCGTG
Stp.aureus	353	CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG
1659 (COMPL)		CGGGAGGCAGCAG
E.colirrsE	407	TATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA - GGGAGTAAAGTTAAT
Cam.jejun5	407	GAGGATGACACTTTTCGGAGCGTAAACTCCTTTCTTAGGGAAG -----AATT
Stp.aureus	415	AGTGATGAAGGTCCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACAATATGTGTAAGTAAC
E.colirrsE	468	ACCTTTGCTCATTTGACGTTACCCGCAGAGAAGCACC GGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5	455	C-----TGACGGTACCTAAGGAATAAGCACC GGCTAACTCCGTGCCAGCAGCCGCG
Stp.aureus	476	-TGTGCACATCTTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B



E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGCGTAAGGGCGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAGCGCGCGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGGAACTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGGTCAATTGGAAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGGTAGAAATTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp-aureus	662	GAGTGCAGAAAGAGGAAAGTGGAATTCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGCGGCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C



E.colirrsE	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
Cam.jejun5	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAGTGTAACCGCTGGGGAGTACGGTCGC
Stp.aureus	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCTGGGGAGTACGACCCG
E.colirrsE	900	AAGGTTAAACTCAAATGAATTGACGGGGGCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Cam.jejun5	876	AAGATTAAACTCAAAGGAATAGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Stp.aureus	909	AAGGTTGAACTCAAAGGAATTGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
E.colirrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGGAAGTTTTTCAGAGATGAGAAAT
Cam.jejun5	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGACAACCTCTAGAGATAGAGCC
E.colirrsE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGA
Cam.jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTCAGCTCGTGTGTGA
Stp.aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCAATGGTTGTCGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrsE	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGG-CC
Stp.aureus	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTAAGCTTAGTTGCCATCA-TTAAAGT-T

FIG. 89D



SB-3 (SEQ ID NO:157)	ATGACGTCAAGTCATC
SB-4 (SEQ ID NO:154)	ATGACGTCAAGTCATC
E.colirrsE	1142 GGGAACCTCAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5	1122 GAGCACTCTAAATAGACTGCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152 GGGCACTCTAAGTTGACTGCCGCTGACAAACCGGAGGAAGGTGGGGATGACGTCAAAATCATC
SB-3	ATGGCCCTTA
SB-4	ATGGCCCTTACGA
E.colirrsE	1204 ATGGCCCTTACGACCAGGGCTACACACGTGCTACAAATGGCGCATACAAAGAGAAGCGACCTC
Cam.jejun5	1183 ATGGCCCTTATGCCCAGGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214 ATGGCCCTTATGATTTGGGCTACACACGTGCTACAAATGGACAATACAAAGGGCAGCGAAACC
E.colirrsE	1266 GCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245 GCGAGGTGGAG-CAAACTCTATAAAATATGTCCAGTTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276 GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328 CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5	1306 CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743(compl)	CGGTGAATACGTTCCCGGGC

FIG. 89E



E.colirrsE	1389	CTTGTAACACCGCCCGTCAACCATGGGAGTGGGTTGCCAAAGAAGTAGGCTTAACCT
Cam.jejun5	1368	CTTGTAACACCGCCCGTCAACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
Stp.aureus	1399	ATTGTACACACCGCCCGTCAACACACGAGAGTTTGTAACACCCCGAAGCCGGTGGAGTAACCT
1743 (compl)		CTTGTAC
E.colirrsE	1451	TCG-GGAGGGCGCTTACCACCTTTGTGATTCACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam.jejun5	1427	AC--T-AGTTACCGTCCACAGTGGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp.aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAAGCCG
E.colirrsE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
Cam.jejun5	1485	TAGGAGAACCTGCGGTTGGATCACCTCCT-----
Stp.aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-

FIG. 89F



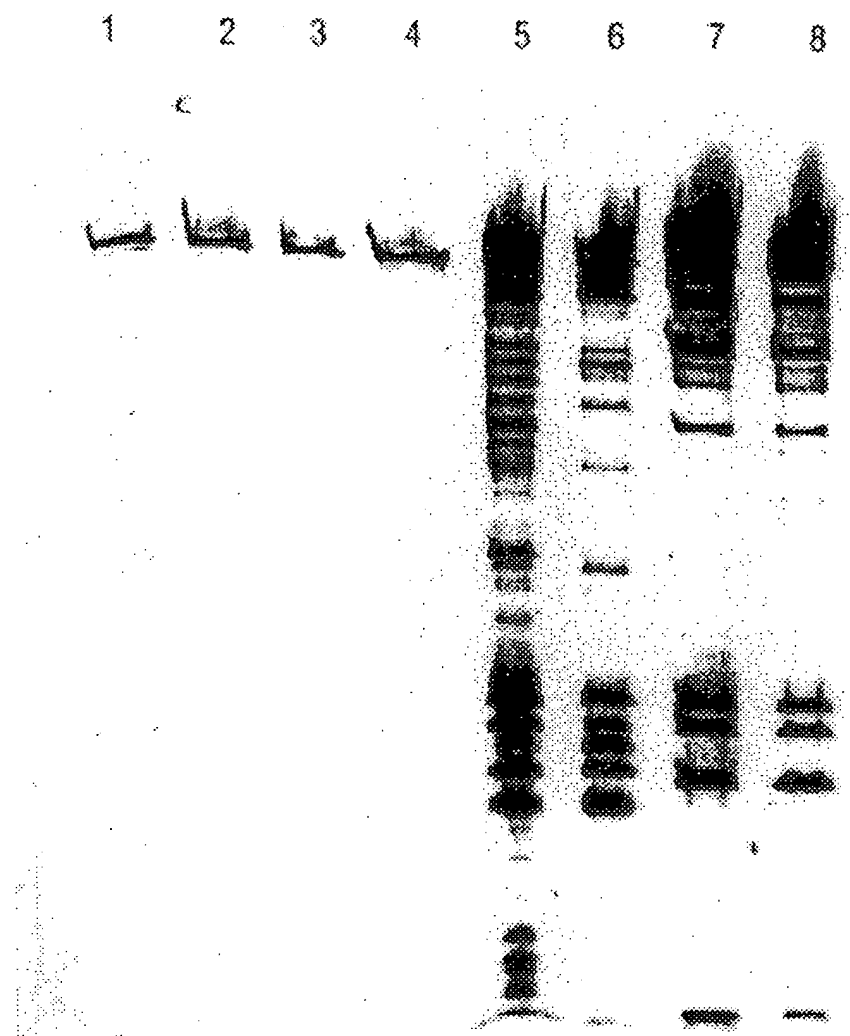


FIG. 90

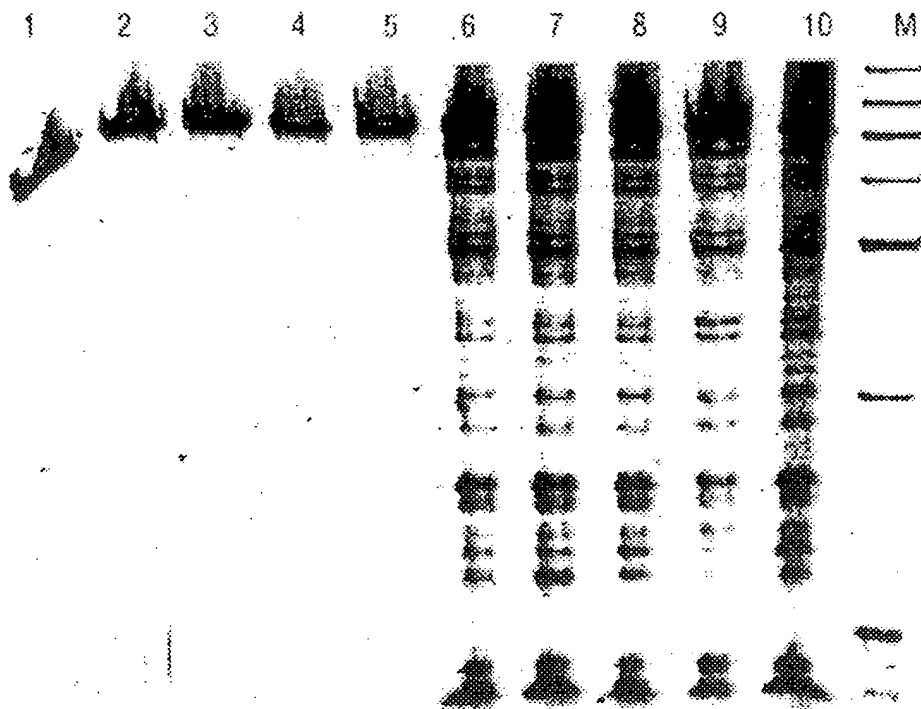


FIG. 91A

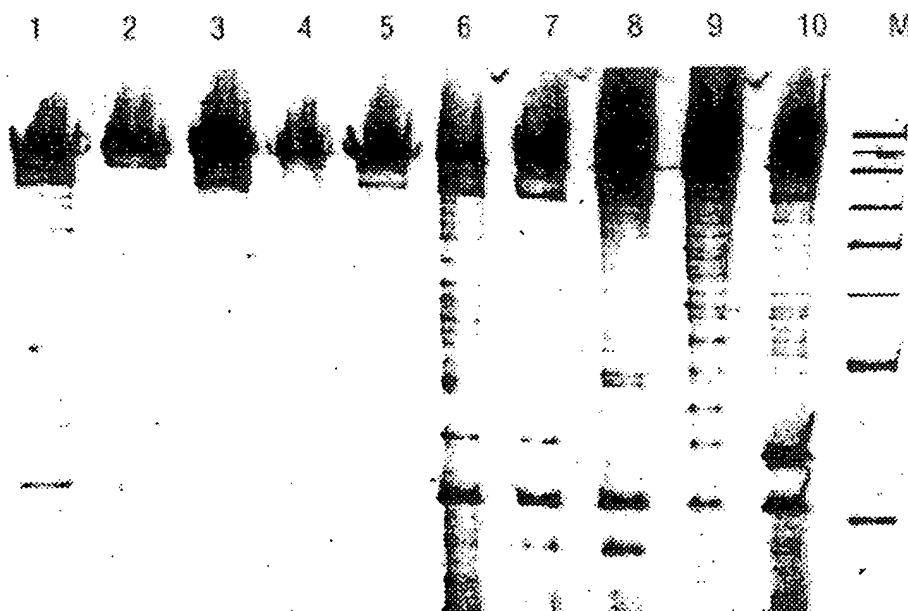
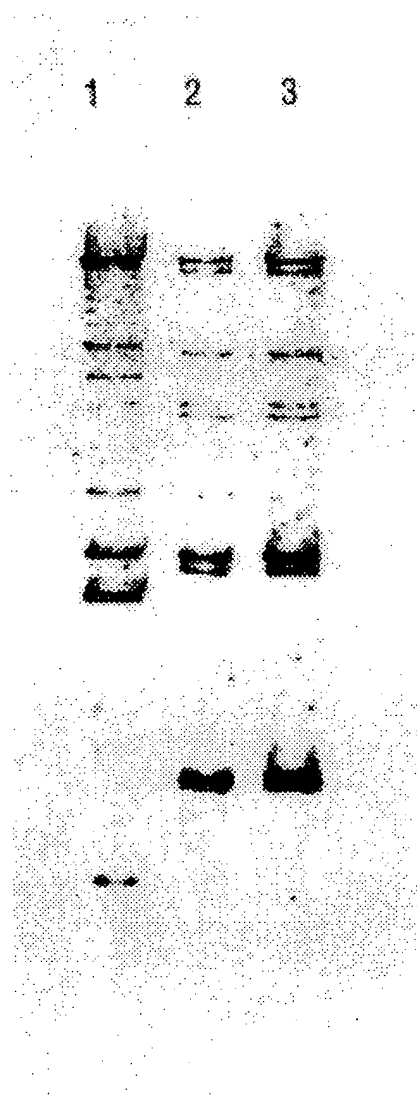


FIG. 91B



**FIG. 92**

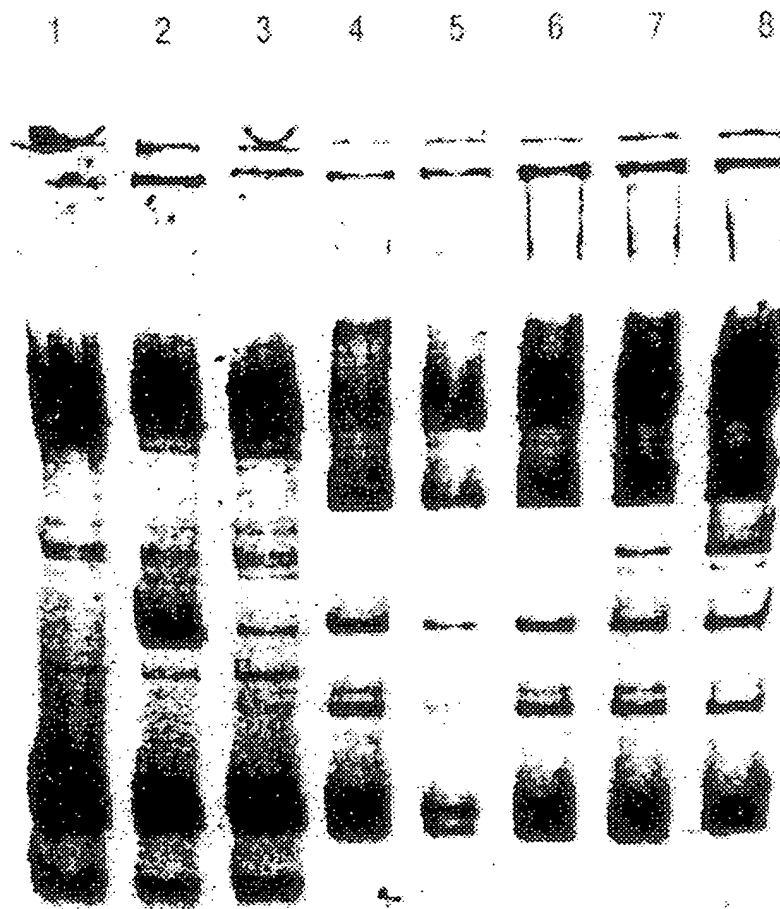


FIG. 93

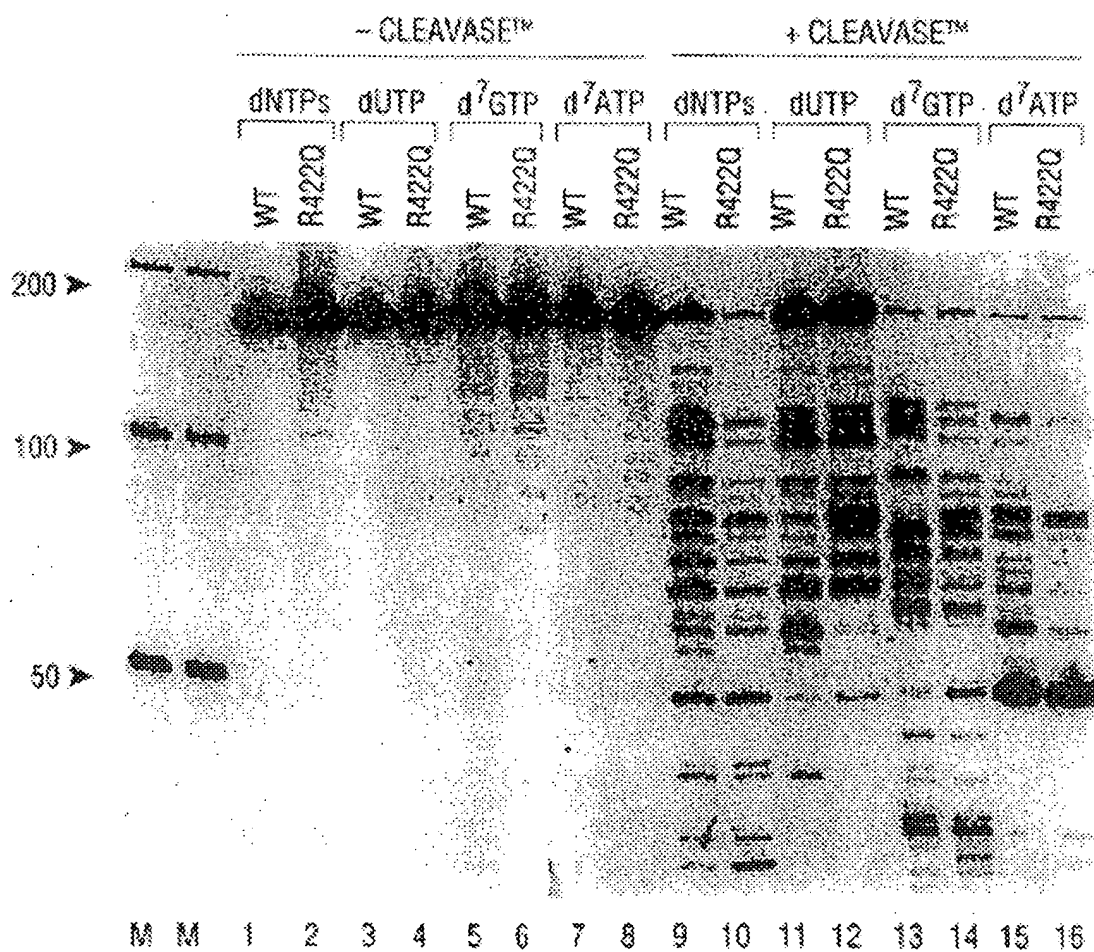


FIG. 94